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O'Rellly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser,A.
INST MEDICAL W & E Hall (AU); PUTHALAKATH HAMSA (AU); REILLY
LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY
SUZANNE (AU); HAMGG DAVID C S (AU); STRASSER ANDREAS (AU)
LOCATION/QUALIFIERS
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Copyright (c) 1993 - 2000 Compugen Ltd.
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O'Rellly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser,A.
Huang,D.C. molecules
Patent: WO 9914321-A 25-WAR-1999;
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY
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Matches 596; Conservative 0; Mismatches 0;
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Matches 596; Conservative 0; Mismatches 0;
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/organism="unidentified"
/do_xref="taxon:32644"
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/note="unnamed protein product"
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0'Connor,L., Strasser,A., O'Reilly,L.A., Hausmann,G., Adams,J.M.,Cory,S. and Huang,D.C.
Cory,S. and Huang,D.C.
Bim: a novel member of the Bcl-2 family that promotes apoptosis
                                                                                                                                                                 '(bases 1 to 597)
'(bases 1 to 597)
'(Connor, L., Strasser, A., O'Reilly, L.A., Hausmann, G., Adams, J.M., O'Connor, L., Strasser, A., O'Cenly, S. and Huang, D.C.S.
Direct Submitssion
Submitted (03-NOV-1997) Molecular Genetics of Cancer, The Walter Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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/note="pro-apoptotic BH3-containing
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100.0%; Pred. No. 2.7e-149;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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/product="Bim-beta1"
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Submitted (06-SEP-2001) Toshiyuki Miyashita, Natlonal Children's
Submitted (06-SEP-2001) Toshiyuki Miyashita, Natlonal Children's
Medical Research Center, Department of Genetics; 3-35-31 Taishido,
Setegada, Toky 154-8509, Japan (E-mail:tmiyashita@nch.go.lp,
Tel:81-3-3414-8121(ex.2763), Fax:81-3-3414-3208)
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PRI
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AB071195-AB071196, AB071198-AB071200"
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llarity 94.8%; Pred. No. 9.2e-138;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Miyashita,T.
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PWSCDKSTQTPSPPCQARNHYLSAMASIROSQEEPEDLRPEIRIAQELRRIGDEFNET
YTRNYFRAEDHPOWYLLOLLFRIFRLVWRR*
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0'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser.A.
Hovel therapeutic molecules
Patent: WO 9914321-A 5 25-MAR-1999;
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); RETLLY
LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY
SUZANNE (AU); HAMGO DAVID C S (AU); STRASSER ANDREAS (AU)
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  Length 722;
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 Score 499.4; DB 9;
Pred. No. 2.2e-123;
0; Mismatches 1;
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/organism="unidentified"
/db_xref="taxon:32644"
1. .>587
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Sequence 5 from Patent W09914321.
AX031283.1 GI:10278614
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83.8%;
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EGNHGGEGDSCPHGSPOGPLAPPASPGPFATRSPLFIFMRRSSLLSRSSSGYFSFDTD
RSPAPMSCDKSTOTPSPPCOAFNHYLSAMASMRQAEPADMRPEINIAQELRRIGDEFN
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Submitted (06-SEP-2001) Toshlyuki Miyashita, National Children's
Submitted (06-SEP-2001) Toshlyuki Miyashita, National Children's
Medical Research Center, Department of Genetics; 3-35-31 Talshido,
Setagaya, Tokyo 154-8509, Japan (E-mail:Emiyashita@nch.go.jp,
Tel:81-3-3414-8121(ex.2763), Fax:81-3-3414-3208)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saplens
Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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0,M., Miyashita,T., Shikama,Y., Tadokozo,K. and Yamada,M.
Molecular cloning and characterization of six novel isoforms of human Bim, a member of the proapoptotic Bcl-2 family(1)
FEBS Lett. 509 (1), 135-141 (2001)
                      ATCTTTATGAGAAGATCCTCCCTGCTGTCTCGATCCTCCAGTGGGTATTTCTCTTTTGAC 300
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Homo saplens mRNA for Bim-alphal, complete cds.
ABO/1195
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gene="bin-alphal"

/note="alternatively spliced: see

AB071196-AB071200"
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/protein_id-"BAB78589.1"
/db_xref-"GI:17351897"
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/db_xref="taxon:9606"
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Miyashita, T.
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                /note="unnamed protein product"
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/db_xref="taxon:32644"
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Matches 523; Conserv
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                                                                                    Caaggtaatcctgaaggcaatcacggaggtgaaggggacagctgccccacggcagcct 180
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                                       Gaps
                                                     CAAGGTAATCCCGACGGC-----GAAGGGGACCGCTGCCCCCACGGCAGCCCT
                                      18;
                      Length 590;
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                      Score 448.4; DB 6;
Pred. No. 1.1e-109;
); Mismatches 61;
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Sequence 5 from Patent W09314321.
AX031309
AX031309.1 GI:10278637
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                      75.2%;
ilarity 86.9%;
Conservative
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unidentified
unclassified.
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BC019556
Mus musculus, BCL2-like 11 (apoptosis facilitator), clone MGC:28730
MAMOE:4459720, mRNA, complete cds.
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/product-"BCL2-like 11 (apoptosis facilitator)*
/protein_id-"AMH19556.1*
/db_xref-"Gr.1945333"
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/translation-"WAKOPSDVSECDREGGGLQPAERPPOLRPCAPTSLQTEDGGNP
DGEGDRCPHGSPQGPLAPPASPGPFATRSPLFIFWRSSLLSRSSGYPSFDTDRSPA
PMSCDRSTOTPSPPGQAFNHYLSAMASIRQSQEEPEDLRPEIRIAQELRRIGDEFNET
TSTRYFANDYREAEDHPOWYLQLLRFIFRLWWRH*

330 c 282 g 250 t
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Eukaryota Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 1137)
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Submitted (19-DEC-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 11 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Conteact: amgebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.W.,
Yoon, V.S., Kowis, C.R., Lawzence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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    Contact: MGC help desk Emall: All Gapbar Gemail. All Government of Gapbar Gemail. All Government of Tissue Procuregent: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.) DNA Sequencing Center.
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Pred. No. 1.1e-109;
0; Mismatches 61;
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/db.xref="Locus1D:12125"
/db.xref="taxon:10090"
/clone="MGC:28730 IMAGE:4459720"
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BC019556.1 GI:18043532
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Bost Local Similarity 86.9%;
Matches 523; Conservative
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DGEGDRCFHGSPGGPLAPPASFGPFATRSPLFIFYRRSSLLSRSSGTFSFDTRRSPA
PMSCDRSTQTPSPPCQAPNHYLSAMASIRQSDEPEDLRPFIRIADELRRIGDERRIGDEFNET
YTRRYFAUDYRABEDHPQMYLQLLRFIFRLVWRRH"
178 c 150 g 125 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 591)
O'Connor,L., Strasser,A., O'Reilly,L.A., Hausmann,G., Adams,J.M.,
O'Connor,L., Strasser, A., O'Reilly,L.A., Hausmann,G., Adams,J.M.,
Cory,S. and Huang,D.C.
Blm: a novel member of the BCl-2 family that promotes apoptosis EMBO J. 17 (2), 384-395 (1998)
                                                                                                                                                                                                                                                                                                                                                                      /note="pro-apoptotic BH3-containing Bcl-2 family member"
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O'Connor_L., Strasser_A., O'Reilly,L.A., Hausmann.G., Adams,J.M.
O'Cy,S. and Huang,D.C.S.
Lord Submission
Submitted (03-NOV-1997) Noiecular Genetics of Cancer, The Walter Eliza Hall institute of Rodical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
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Pred. No. 1.1e-109;
0; Mismatches 61; Indels 18;
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1. .591
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                                                                                                                                                                                                                                                                                                                                                                                                         /product="BimEL"
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Best Local Similarity 86.9%;
Matches 523; Conservative
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/Organism="Rattus norvegicus"

/db_xref="taxon:10116"

1. :591
/codon_start=1
/codon_start=1
/product_"Bol: 2 related ovarian death gene product BOD-L"
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OGEOINCPHGSPOGPLAPPASPOGPFARRSPLIFVRRSSLLSRSSGOYFSPOTDRSPA
PMSCOKSTOTESPROGAPNIFLSAMASIRGSGEPEDLRFEIRIAGELRRIGDEFNET
YTRRAFANDYERAEDHOWYLLQLLREIFRLWHRRH"

39 a 177 c 153 g 122 t
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Pred. No. 2.1e-108;
0; Mismatches 64; I
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Sciurognathi; Muridae; Murinae;
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of
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Hsu.S.Y., Lin.P. and Hsueh, A.J.
BOD (Bcl-2-related ovarian death gene) is an ovarian E
domain-containing proapoptotic Bcl-2 protein capable of
dimerization with diverse antiapoptotic Bcl-2 members
Mol. Endocrinol. 12 (9), 1432-1440 (1998)
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Hau, S.Y. and Hsueh, A.J.W.
Direct Submission
Submitted (15-MAY-1998) GYN/OB, St
Stanford, CA 94305, USA
Location/Qualifiers
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Bcl-2 related
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Rattus norvegicus Bc
mRNA, complete cds.
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              18;
Length 591;
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AB071198.1 GI:17351902
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Direct Submission
Submitted (19-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 5108, USA
On Sep 19, 2001 this sequence version replaced 91:7248987.
                                                                     Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 181497)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                /clone="RP11-438K19"
40542 c 39097 g 49529
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1. 181497
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/chromosome="2"
   AC096670 AC013332
AC096670.1 GI:15668150
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Waterston, R.H.
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                                                           Homo sapiens
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                                                                                                                                        Direct Submission
Submitted (06-SEP-2001) Toshiyuki Miyashita, National Children's
Medical Research Center, Department of Genetics; 3-35-31 Taishido,
Setagaya, Tokyo 154-8509, Japan (E-mail:tmiyashita@nch.go.jp,
Tel:81-3-344-8121(ex.2763), Fax:81-3-3414-3208)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
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                          l (sites)
U,M., Miyashita,T., Shikama,Y., Tadokoro,K. and Yamada,M.
Molecular cloning and characterization of six novel isoforms imman Bim, a member of the proapoptotic Bcl-2 family(1)
FEBS Lett. 509 (1), 135-141 (2001)
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. .408
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Miyashita, T.
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                                  0; Gaps
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Ouery Match
66.2%; Score 394.4; DB 9; Length 181497;
Best Local Similarity 99.7%; Pred. Mo. 3.9e-95;
Matches 395; Conservative 0; Mismatches 1; Indels 0;
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482

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Submitted (03-NOV-1997) Molecular Genetics of Cancer, The Walter & Submitted (03-NOV-1997) Molecular Genetics of Cancer, The Walter & Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia

Location/Qualifiers

1. 417

//Organism="Homo sapiens"

//db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

O'Connor.L., Strasser.A., O'Reilly,L.A., Hausmann,G., Adams,J.M.,

Gory,S. and Huang,D.C.

EMBO 3, 17 (2), 384-395 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 417)
O'Connor,L., Strasser,A., O'Rellly,L.A., Hausmann,G., Adams,J.M.,
Cory,S. and Huang,D.C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY SUZANNE (AU); HUANG DAVID C S (AU); STRASSER ANDREAS (AU) LOCATIOn/Qualifilers
                                                                                                                                                                                                                                                                                                                                                                                                                                               303 agacaggagcccagcacccatgagttgtgacaatcaacacaaaccccaagtcctccttg 362
                                                                                                                                                                                                                                                                                                                                                                                                 143 TATECGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGGTATCGGAGACGAGTTTAACGC 302
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/note="unnamed protein product"
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                                                       1. .416
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AF032458
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   PAT 20-SEP-2000
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Batent: WO 9914317 m 7 25-WAR-1999;
INST WEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY SUZANNE (AU); HAMSD DAVID C S (AU); STRASSER ANDREAS (AU)
Location/Qualifiers
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O'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser,A.
Huang,D.C. and Strasser,A.
Novel therapeutic molecules
Patent: WO 99143121-A 25-WAR-1999;
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 TATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATCGGAGACCAGTTTAACGC 302
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AX031285 416 bp
Sequence 7 from Patent W09914321.
AX031285 GI:10278616

    416
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Best Local Similarity 100.0%; Pred. No. 2.9e-68;
Matches 294; Conservative 0; Mismatches 0;
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Human breast cell
Human foetal liver
Probe #1601 for ge
Human bone marrow
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Probe #1578 used t
Probe #1243 used ge
Human bone marrow
Probe #1243 used ge
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Human reproductive
Drosophila melanog
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AAI3655
AAK313656
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Puthalakath H, Strasser A;
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97AU-0009263
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  Homo sapiens.
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17-SEP-1997;
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                                                                          August 7, 2002, 19:36:18 ; Search time 210.72 Seconds (Without alignments) 4856.117 Million cell updates/sec
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Human Bcl-2 inter
Human Bcl-2 intera
DNA encoding novel
Murine Bcl-2 inter
Human polypuclecti
Human Jurkat cell
Human Jurkat cell
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1: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*

2: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*

3: /SIDSI/gcgdata/geneseqn-embl/NA1982.DAT:*

4: /SIDSI/gcgdata/geneseqn-embl/NA1983.DAT:*

5: /SIDSI/gcgdata/geneseqn-embl/NA1983.DAT:*

6: /SIDSI/gcgdata/geneseqn-embl/NA1986.DAT:*

7: /SIDSI/gcgdata/geneseqn-embl/NA1986.DAT:*

8: /SIDSI/gcgdata/geneseqn-embl/NA1986.DAT:*

8: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*

9: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*

10: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*

11: /SIDSI/gcgdata/geneseqn-embl/NA1980.DAT:*

12: /SIDSI/gcgdata/geneseqn-embl/NA1990.DAT:*

13: /SIDSI/gcgdata/geneseqn-embl/NA1990.DAT:*

14: /SIDSI/gcgdata/geneseqn-embl/NA1990.DAT:*

15: /SIDSI/gcgdata/geneseqn-embl/NA1991.DAT:*

16: /SIDSI/gcgdata/geneseqn-embl/NA1991.DAT:*

17: /SIDSI/gcgdata/geneseqn-embl/NA1991.DAT:*

18: /SIDSI/gcgdata/geneseqn-embl/NA1991.DAT:*

19: /SIDSI/gcgdata/geneseqn-embl/NA1991.DAT:*

10: /SIDSI/gcgdata/geneseqn-embl/NA2001.DAT:*

11: /SIDSI/gcgdata/geneseqn-embl/NA2001.DAT:*

12: /SIDSI/gcgdata/geneseqn-embl/NA2001.DAT:*

13: /SIDSI/gcgdata/geneseqn-embl/NA2011.DAT:*

14: /SIDSI/gcgdata/geneseqn-embl/NA2001.DAT:*
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                                                                                                                                               1 atggcaaagcaaccttctga.......tggtgtggagaatgcattg 596
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           4.5
Compugen Ltd.
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                                                                                                                                                                                                       1736436 segs, 858457221 residues
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            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAX24995
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                                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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590
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Post-processing:

Database

Perfect score: Scoring table:

Sequence:

Searched:

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OM nucleic

Run on:

WPI; 1999-244030/20.

596 448.4 294 276 207.6 127 71 37

98465 υv

Result No.

Thu Aug

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The present sequence encodes the extra long form (EL) of human Bim, or Bel-2 interacting mediator of cell death (see AAW89158), a novel member of the Bel-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bel-2 family. Bim is a BH3-only protein, as the only Bel-2 homology region which it encompasses is BH3. It is the only BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. Bim-5, Bum-1, and Bim-EL. and Bim-EL. and Bim-EL. and Bim-EL. and Bim-EL. and Bim-EL and Bim-EL and Bim-EL at bands 2012-2013. Binding the dynean light chrowse blm cDNA. Murline Bim-3, Binding the dynean light chrowse blm cDNA. Murline Bim-3 bunca and liver cDNA libraries using mouse blm cDNA. Murline Bim-3, Binding the dynean light chrowse blm cDNA and Sq12-2013. Binding the dynean light chrowse botten killer than either Bim-10 bim. Bim-3.

EC chain was shown to regulate the pro-apoptotic activity of Bim. Bim-5, the splice variant which does not bind to dynein light chain is a much more potent killer than either Bim-10. Bim-EL. The Invention provides variants (see AAW89159-68) of murine and human bim-10. Bim-10. The line crannel bind, couple or othervise associate with a dynein light chain. The identification of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act useful in cancer, autoimmune or degenerative disease therapeut concerns of Bim activity is useful in regulating inhibition or streament or prophlastats in conditions such as cancer and delection of autoreactive lymphocytes in autoimmune of bisease. Decreased Bim expression of Bim activity is useful in regulating inhibition of preventions during e.g. gamma-involving the survival of conditions during e.g. gamma-involving the survival of conditions during e.g. gamma-involving the survival of preventing generation of fertile sperm.

EVERT
                                                 New isolated member of the Bcl-2 family, Bim used in, e.g. cancer
                                                                                                                            Claim 7; Page 101-102; 145pp; English.
P-PSDB; AAW98158.
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Sequence 596 BP; 145 A; 175 C; 146 G; 130 T; 0 other;

ö cagggcccgctggccccacctgccagccttggctaccagatccccgctttc 240 cagggcccgctggccccacctgccagccctggcccttttgctaccagatccccgctttc 240 acagacagagacccagcaccatgagttgtgacaaatcaacacaaaccccaagtcctcct 360 Indels 0; Gaps 100.0%; Score 596; DB 20; Length 596; 100.0%; Pred. No. 4.3e-178; 1.1ve 0; Mismatches 0; Indels 0; Query Match Best Local Similarity 100.0 Matches 596; Conservative 61 61 121 121 181 181 241 241 301 ŝ 윱 ð 셤 õ g ò 셤 ð 8

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The present sequence encodes the extra long form (EL) of murine Bin, or BG1-2 interacting mediator of cell death (see AAW9B156), a novel member of the BG1-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival BG1-2 family. Bin is a BH3-only protein, as the only BG1-2 homology region which it encompasses is BH3. It is the only BH3-only protein for which splice variants exist. These result in the expression of a wariety of !soforms, i.e. Bin-S. Bin-L and Bin-EL (see AAW9B154-56). CDNAs encoding these murine Bin isoforms were obtained from a T lymphoma cDNA library using human recombinant Bc1-2 protein. The murine Bin gane has been mapped to chromosome 2 at bands F3-G. Human Bin-L and Bin-El isoforms have combinant Bc1-2 protein. The murine Bin gene has been mapped to chromosome 2 at bands F3-G. Human Bin-L and Bin-El isoforms have chain was shown to require the pro-apoptotic activity of Bin. Bin-S, the splice variant which does not bind to dynein light
                                  421 gatatgcgcccagagatatggatcgcccaagagttgcggcgtatcggagacggtttaac 480
                                                                                                                                                                                481 gcttactatgcaaggaggqtattttgaataattaccaagcagccgaagaccaccacga 540
                                                                                                                                            421 gatatgcgcccagagatatggatcgcccaagagttgcggcgtatcggagacgagtttaac 480
                                                                                                                                                                                                                  481 gcttactatgcaaggagggtattttgaataattaccaagccgaagaccaccacga 540
301 acagacaggagcccagcacccatgagttgtgacaaatcaacacaaaccccaagtcctcct 360
                                                                                                                                                                                                                                                     New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bim-EL; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine Bcl-2 interacting mediator of cell death Bim-EL cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 96-97; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 AAX24995 standard; cDNA; 590 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-AU00772.
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Puthalakath H, Strasser A;
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P-PSDB; AAW98156.
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17-SEP-1997;
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The invention provides variants (see AAM98159-68) of murine and human Bin-Lor Bin-EL.

The invention provides variants (see AAM98159-68) of murine and human Bin-Lor Bin-EL that cannot bind, couple or otherwise associate with a dynein light chain. The identification of Bim permits the identification and rational design of a range of products for use in therapp, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antagonists or agonists of Bim's function and will be useful in cancer, autoimmune or degenerative disease therapy. Increased Bim expression or Bim activity is useful, e.g. for treatment or prophylaxis in conditions such as cancer and deletion of autoreactive lymphocytes in autoimmune disease. Decreased Bim expression of Bim activity is useful in regulating inhibition or prophylaxis in conditions such as under cytotoxic conditions during e.g. gamma-irradiation and chemotherapy or during HIV/AIDS or other viral infections, ischemia, myocardial infarction, cells being transplanted for treatment of diseases. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity is useful. e.g. as a contraceptive or method of sterilization by is useful, e.g. as a contraceptive or m preventing generation of fertile sperm.

Sequence 590 BP; 137 A; 178 C; 150 G; 125 T; 0 other;

ö 241 atctttatgagaagatcctcctgctgtctcgatcctccagtgggtatttctttttgac 300 121 caaggtaatcctgaaggcaatcacggaggtgaaggggacagctgcccccacggcagcct 180 CCtgcagatatgcgcccagagatatggatcgcccaagagttgcggcgtatcggagacgag 474 cctgaagatctgcgcccggagatacggattgcacaggagctgcggcggatcggagacgag 468 tttaacgettactatgcaaggaggtatttttgaataattaccaagcagccgaagaccae 534 18; Gaps 75.2%; Score 448.4; DB 20; Length 590; llarity 86.9%; Pred. No. 1.9e-131; Conservative 0; Mismatches 61; Indels 18; Query Match Best Local Similarity Matches 523; Conserv tg 596 301 289 361 349 415 409 475 469 535 529 595 g g ò g å Q ò g ò g ò 용 ò 8 ò g õ 8 õ ŝ ô

290

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589

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The present sequence encodes the long form (L) of human Bim, or Bcl-2 interacting mediator of cell death (see AAW98157), a novel member of the Bcl-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bcl-2 family. Bim is a BH3-only protein as the only Bcl-2 homology region which it encompasses is BH3. It is the only Bcl-2 homology region which it encompasses is BH3. It is the only BH3-only protein for which splice variants exist. These colly Bcl-2 homology region which it encompasses is BH3. It is the only BH3-only protein for which splice variants exist. These call be and be splice variety of isoforms, i.e. Bim-5. Bim-5. Bim-1. AAW98158) were isolated from embryo and liver conva libraries using mouse blin cDNA. Murine Bim-5, Bim-1 and Bim-2. Isoforms (see AAW98154-56) are also provided. The human Bim gene maps to chain was shown to regulate the pro-apoptotic activity of Bim.

AAW98154-56) are also provided. The human Bim gene maps to chain was shown to regulate the pro-apoptotic activity of Bim.

Bim-5, the splice variant which does not bind to dynein light chain, is a much more potent killer than either Bim-1 or Bim-EL.

The invention provides variants (see AAW98159-68) of murine and human Bim-1. Or Bim-EL that cannot bind, couple or otherwise associate with a dynein light chain. The identification of Bim permits the identification and rational design of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antagonists or agonists of Bim's function and will be useful in cancer, autoimmune of generative disease. Decreased Bim crepression of Bim activity is useful, e.g. for treatment or prophylaxis in autoimmune disease.

Conditions during e.g. gamma-irradiation and chemotherapy or during Hypological antagonars or for prophylaxis in conditions such as sunder cytotoxic conditions are diseases or for prologonary desen
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                                                                                                                                                                                                          Bim-L; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle; human; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                                                                                  Human Bcl-2 interacting mediator of cell death Bim-L cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Connor L, O'Reilly L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 99-100; 145pp; English.
                                          AAX24996 standard; cDNA; 416 BP.
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Puthalakath H, Strasser A;
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                                                                                                                       05-JUL-1999 (first entry)
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P-PSDB; AAW98157.
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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17-SEP-1997;
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                                                                                  AAX24996;
RESULT
AAX24996
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                                                                                                                                                                                        423 tatgogoccagagatatggatogoccaagagttgoggogtatoggagacgagtttaacgo 482
                                                                                                                                                     303 agacaggagcccagcacccatgagttgtgacaaatcaacacaaaccccaagtcctccttg 362
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy, forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
expressed in germ cells, modulating Bim expression or Bim activity its useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                     49.3%: Score 294; DB 20; Length 416; 100.0%; Pred, No. 1e-82; ive 0; Mismatches 0; Indels
                                                 Sequence 416 BP; 113 A; 113 C; 103 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 1154; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS65350 standard; cDNA; 442 BP
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23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002 (first entry)
                                                                                    Query Match
Best Local Similarity 100.0
Matches 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
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P-PSDB; ABG01163.
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and gene mapping, and in recombinant production of (11). The copincides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene thrapy techniques of the restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating casing of sites expressing (11). (1) and (11) are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating cason and polyuncleotide sequences have applications in the polypeptide and polyuncleotide sequences have applications in the polypeptide and polyuncleotide sequences have applications in and to produce other types of data and products dependent on DNA and to praduce other types of data and products dependent on DNA and canno acid sequences. A&Sé4197-A&S4564 represent novel human configuration. But was obtained in electronic format directly from WIPO very
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                                                                                                                                                                                                                                                                                                                                                                                        Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                            Length 442;
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                                                                                                                                                                                                                                                                                                                                                       Query Match 46.3%; Score 276; DB 23; Best Local Similarity 100.0%; Pred. No. 5.1e-77; Matches 276; Conservative 0; Mismatches 0;
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17-SEP-1997;
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The present sequence encodes the long form (L) of murine Bim, or member of the Bol-2 family that is capable of inducing cell death (see AAW98155), a novel member of the Bol-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of fapoptosis) and which acts as a' death-ligand' for certain members only Bel-2 homology region which it encompasses is BH3. It is the only Bel-2 homology region which it encompasses is BH3. It is the conly BH3-only protein for which splice variants exist. These result in the expression of a variety of soforms, i.e. Bin=5.

Bim-L and Bim-EL (see AAW98154-56). CDNAs encoding these murine Bim recombinant Bel-2 protein. The murine Bim gene has been mapped to chromosome 2 at bands F3-6. Human Bim-L and Bim-EL isoforms have a look of see AAW98157-58). Binding the dynein light chain was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan was shown to requilate the pro-apoptotic activity of Bim. Collan bim. Collan was shown to action of Bim permits the invention provides variant which does not bind to dynein light chain. The latentification and involving modulation of physiological cell death. These therapeutic molecules may act the threapy, dagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act settler anteaponists or agonists of some such activity is useful in requilating inhibition or coll death or degeneration and encoderation and encoderation and encoderation and encoderation and encoderation and encoderation w
                                                                                                                                                                                            New isolated member of the Bcl-2 family, Bim used in, e.g. cancer
                                              Adams J, Cory S, Huang DCS, O'Connor L, O'Reilly L;
Puthalakath H, Strasser A;
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                              Claim 3; Page 94-95; 145pp; English.
                                                                                                                WPI: 1999-244030/20.
P-PSDB; AAW98155.
                                                                                                                                                                                                                     treatment
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; ccaggecttcaaccactatetcagtgcaatggcttccatgaggcagget----gaacc 416 taacgettactatgeaaggaggtattttgaataattaceaageageegaageee 536 6; Gaps Ouery Match 34.8%; Score 207.6; DB 20; Length 422; Best Local Similarity 83.3%; Pred. No. 2.1e-55; Matches 250; Conservative 0; Mismatches 44; Indels 6; Sequence 422 BP; 112 A; 116 C; 109 G; 85 T; 0 other; 303 363 183 243 477 303 417

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537 acgaatggttatcttacgactgttacgttacattgtccgcctggtggagaatgcattg 596
        New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment
                                                                                                               Bim-S; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                 Murine Bcl-2 interacting mediator of cell death Bim-S cDNA.
                                                                                                                                                                                                                                                          Adams J, Cory S, Huang DCS, O'Connor L, O'Rellly L; Puthalakath H, Strasser A;
                                                                                                                                                                                                                                          (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                    AAX24993 standard; cDNA; 332 BP.
                                                                                                                                                                                                                   97AU-0009373.
97AU-0009263.
                                                                                                                                                                                                     98WO-AU00772.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                              WPI; 1999-244030/20.
P-PSDB; AAW98154.
                                                                                                                                                       Mus musculus.
                                                                                                                                                                      W09914321-A1.
                                                                                                                                                                                                    17-SEP-1998;
                                                                                                                                                                                                                    24-SEP-1997;
                                                                                                                                                                                                                            17-SEP-1997;
                                                                                                                                         isoform; ss.
                                                                                  05-JUL-1999
                                                                                                                                                                                     25-MAR-1999
                                                                   AAX24993;
                                             AAX24993
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The present sequence encodes the short form (S) of murine bim, or mediator of cell death (see AAW98154), a novel member of the BC1-2 family that is capable of inducing cell death embers of concentration and which acts as a 'death-ligand' for certain members of the BC1-2 hamily that is capable of inducing cell death as the concentration and which acts as a 'death-ligand' for certain members of the pro-survival BC1-2 family. Bim is a BH3-only protein, as the only BC1-2 homology region which the correspasses is BH3. It is the only BH3-only protein for which splice variants exist. These conly BC1-2 homology region of a variety of isoforms, i.e. Bim-5. Bim-EL and Bim-EL (see AAW98154-56). CDNAs encoding these murine Bim isoforms were obtained from a T lymphoma cDNA library using human concombinant BC1-2 protein. The murine BIM gene has been mapped to chromosome 2 at bands F3-G. Human BIM-L and BIM-EL isoforms have also been identified (see AAW98157-58). Binding the dynain light chromosome 2 at bands F3-G. Human BIM-L and BIM-EL isoforms have also been identified the pro-apoptotic activity of BIM.

Chromosome 2 at bands F3-G. Human BIM-L and BIM-EL isoforms have also been identified the pro-apoptotic activity of BIM.

Chromosome 2 at bands F3-G. Human BIM-L and BIM-EL isoforms have also much more potent Killer than either BIM-L or BIM-EL.

Chain, is a much more potent Killer than either BIM-L or BIM-EL.

Chain, is a much more potent Killer than either BIM-L or BIM-EL.

Chain, is a much more potent Killer than either BIM-E.

Chain, is a much more potent Killer than either BIM-E.

Chain, is a much more potent Killer than either BIM-E.

Chain, is a much more potent Killer than either BIM-E.

Chain, is a much moral design of a range of products for use the interaction and rational design of a range of products for use in therapy diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antegionists or agonists of BIM's function and value more concen

Claim 3; Page 92; 145pp; English.

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586 agaatgcattg 596
                                                                                                                                                                                                                                                                                   311 AGAATGCATTG 301
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                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                            AAZ38853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                caggctgaacctgcagatatgcgcccagagatatggatcgcccaagagttgcggcgtatc 465
                                                                                                                                                                                                          ggagacgagtttaacgettactatgcaaggagggtattttgaataattaccaagcagec 525
                                                                                                                                                                                                                      142 caggaggaacctgaagatctgcgcccggagatacggattgcacaggagctgcggcggatc 201
                                                                                                                                           Gaps
conditions during e.g. gamma-irradiation and chemotherapy or during HTVAIDS or other viral infections, ischemia, myocardial infarction, hypoxia, degenerative diseases or for prolonging the survival of cells being transplanted for treatment of disease. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity is useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                     21.3%; Score 127; DB 20; Length 332; 79.1%; Pred. No. 5.5e-30; ive 0; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 9344; 1399pp + Sequence Listing; English.
                                                                                      Sequence 332 BP; 87 A; 85 C; 91 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 9344.
                                                                                                                                                                                                                                                                                                                                                                     AAI89284 standard; cDNA; 371 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                Best Local Similarity 79.1
Matches 151; Conservative
                                                                                                                                                                                                                                                                                             586 agaatgcattg 596
                                                                                                                                                                                                                                                                                                                 agaaggcattg 332
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P-PSDB; AAO09353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                                                                                                                                                                           AA189284;
                                                                                                                     Query Match
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cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, Jurkat cell; tumour necrosis factor receptor releasing enzyme; TRRE; oytokine; TRF; identification; cytostatic; anti-inflamatory; cardiant; immunomodulator; antiarthritts; antibacterial; cancer; heart failure; cachexia; inflammation; endotoxic shock; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Jurkat cell clone 2-9 AIM2 which affects TRRE activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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2.9e-12;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 371 BP; 106 A; 95 C; 81 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 71; DB 100.0%; Pred. No. 2.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA238853 standard; DNA; 4047 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; sepsis; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 71; Conservative
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assess a disease condition associated with altered TRRE activity. The polypebtides, polynucleotides and antibodies can be used to decrease or increase signal transduction from a cytokine in a cell. The polypeptides, polynucleotides and antibodies may be used to treat heart failure, cachexia, inflammation, endotoxic shock, arthritis, multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes isolated polynucleotides (A) comprising a sequence expressed at the mRNA level in Jurkat T cells and showing increased enzymatic activity for cleaving and releasing the tumour
                                                                                                                                                                                                                                 203 canadocaccocaccacacacacacacacacacanacanagacacacacaracana 144
                                                                                                                                                                                                                                                                                              125 gtaatcctgaaggcaatcacggaggtgaaggggacagctgccccacggcagcctcagg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Jurkat cell; tumour necrosis factor receptor releasing enzyme; TRRE; cytokine; TNF; identification; cytostatic; anti-inflammatory; cardiant; immunomodulator; antiarthritic; antibacterial; cancer; heart failure; cachexia; inflammation; endotoxic shock; arthritis; multiple sclerosis; sepsis; ds.
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/note- 'longest open reading frame in the AIM2 clone"
                                                                                                                                                                                                   Caps
                                                                                                                                                                                                                                                                                                                    143 GAGTGGCGGCCCCCAGCTGGAGGGCGCCCCCAGCCCTCCCCAGC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Jurkat cell clone 2-9 AIM2 complementary nucleotide strand.
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                                                                                                                                                              Ouery Match 6.2%; Score 37; DB 21; Length 4047; Best Local Similarity 52.2%; Pred. No. 0.49; Matches 82; Conservative 0; Mismatches 75; Indels (
                                                                                                              Sequence 4047 BP; 846 A; 1023 C; 1278 G; 900 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                  185 gecegetggececacetgecagecetggecettttge 221
                                                                                                                                                                                                                                                                                                                                                                                      83 CCACTCTGGCCCCGCAGCCCCCCTGGTCCGAGTGC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 94-96; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
378..1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA238863 standard; DNA; 4047
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                                                                               and sepsis, and cancer
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P-PSDB; AAX56509.
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necrosis factor (TNF) receptor in genetically modified COS-1 cells expressing the receptor. Methods from the present invention can be used to assess a disease condition associated with altered TRRE activity. The polypeptides, polynucleotides and antibodies can be used to decrease or increase signal transduction from a cytokine in a cell. The polypeptides, polynucleotides and antibodies may be used to treat heart failure, cachexia, inflammation, endotoxic shock, arthritis, multiple sclerosis and sepsis, and cancer. The present sequence represents the complementary strand of the AIMZ clone which affects tumour necrosis factor receptor releasing enzyme (TRRE) activity, which encodes the longest open reading frame shown in AAV56509.
                                                                                                                                                                                                                                                                                                                                                                                                         3845 cgaggccgcccgccggggccccacgcgggccccatccgcaggccaggactgccttcccg 3904
                                                                                                                                                                                                                                                                                                                125 gtaatcctgaaggcaatcacggaggtgaaggggacagctgccccacggcagccctcagg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                  6.2%; Score 37; DB 21; Length 4047; 52.2%; Pred. No. 0.49; tive 0; Mismatches 75; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1629; 327pp + sequence listing; English.
                                                                                                                                                                                                  Sequence 4047 BP; 900 A; 1278 C; 1023 G; 846 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast cell single exon nucleic acid probe #1629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3965 ccactetggccccgcagccccgcctggtccgagtgc 4001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 gccgctggcccacctgccagcctggcccttttgc 221
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-023689.
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                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; cancer; ss.
                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 82; Conserv
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 gtaatcctgaaggcaatcacggaggtgaaggggacagctgcccccacggcagcctcagg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 tgcatccgccacgtcttcacctaggggagcagccagtgggccccagtgcacagcgtcccg 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 cgccgtggacttgaccacccagagcagtgcatgcagcccagctggatgcaggtgaacaga 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #1601 for gene expression analysis in human heart cell sample.
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                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                   Length 480;
                                                                                                                           Claim 1; SEQ ID NO 1660; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                Sequence 480 BP; 109 A; 162 C; 129 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
6.2%; Score 36.%; DB 22;
Best Local Similarity 50.0%; Pred. No. 0.21;
Matches 92; Conservative 0; Mismatches 92;
         Rank DR;
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       Chen W,
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2000us-0207456.
2000us-0612366.
2000us-023366.
2000us-0236359.
2000us-0236359.
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         Penn SG, Hanzel DK,
                                         WPI; 2001-483447/52.
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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The invention relates to a spatially-addressable set of single exon chuclet caid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label carried from mRNA of human breast, and then measuring the label carried from mRNA of human breast, and then measuring the label carried from mRNA of human breast, and then measuring the label carried from mRNA of human breast, and then measuring the label carried from probes of the microarray. The probes are useful for second procession of carried from an expression analysis is useful for assessing the toxicity of chemical captures on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed expence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the prince of from MIPO at fip.wlpo.int/pub/published_pct_sequences.
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2000US-0207456.
2000US-0608408.
2000US-05324687.
2000US-0234687.
2000US-0234587.
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26-MAY-2000;
30-JUN-2000;
03-MG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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202 atat 205
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03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234697.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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26-MAY-2000; 2000US-0200
30-JUN-2000; 2000US-060B40B
03-AUG-2000; 2000US-0632366.
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Best Local Similarity 50.0%
Matches 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                              measuring human gene expression in sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart on vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                        Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                       The present invention relates to single exon nucleic acid probes for
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50.0%; Pred. No. 0.21;
tive 0; Mismatches 92;
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                                                                                                              Claim 1; SEQ ID No 1601; 530pp; English.
                        Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC.
                        Chen W,
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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Best Local Similarity 50.0
Matches 92; Conservative
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                        Hanzel DK,
                                             WPI; 2001-488899/53
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                        Penn SG,
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheiner's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 1613; 650pp + Sequence Listing; English.
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Pred. No. 0.21;
0; Mismatches 92;
                                                               Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC
                                                               Penn SG, Hanzel DK, Chen W,
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Search completed: August 7, 2002, 20:43:57 Job time: 4059 sec
  04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #1595 for gene expression analysis in human cervical cell sample.
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Pred. No. 0.21;
0; Mismatches 92; Indels 0;
                                                                                                                                             Example 4; SEQ ID NO: 1621; 658pp + Sequence Listing; English.
                                                                                                            Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                              Sequence 480 BP; 109 A; 162 C; 129 G; 80 T; 0 other;
                                                                  Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                    .
                                            (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI11662 standard; DNA; 480 BP
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                          Local Similarity 50.0
les 92; Conservative
                                                                  Hanzel DK,
                                                                                       WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 ttat 248
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                  Penn SG,
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Best Local Si
Matches 92;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 gtaatcotgaaggcaatcacggaggtgaaggggacagctgccccacggcagcctcagg 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 tgcatccgccacgtcttcacctaggggagcagccagtgggccccagtgcacagcgtcccg 141
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                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 6.2%; Score 36.8; DB 22; Length 480; Local Similarity 50.0%; Pred. No. 0.21; nes 92; Conservative 0; Mismatches 92; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 480 BP; 109 A; 162 C; 129 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID No 1595; 487pp; English.
                                                                              Chen W, Rank DR;
(MOLE-) MOLECULAR DYNAMICS INC.
                                                                              Penn SG, Hanzel DK,
                                                                                                                                                   WPI; 2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                    US-08-184 3274 32

US-08-184 3274 32

US-08-06-01-15

US-08-06-00-075-3

US-08-09-075-3

US-09-38 - 586-27

US-09-38 - 586-27

US-09-38 - 586-27

US-09-390-379-1

US-08-990-379-1

US-08-990-379-1

US-08-990-379-1

US-08-990-379-1

US-08-980-379-1

US-08-884-363-1

US-08-884-363-1

US-08-884-363-1

US-08-884-363-1

US-08-884-363-1

US-08-884-2276-13
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILLING DATE: 26-806-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463; Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703)00.
TELERAX: (703)00.
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Single
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US-08-232-463-14
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Sequence 5, Appl
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596
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1. /cgn2_6/ptodate/1/ina/5A_COMB.seq:*
22. /cgn2_6/ptodate/1/ina/6B_COMB.seq:*
33. /cgn2_6/ptodate/1/ina/6A_COMB.seq:*
4. /cgn2_6/ptodate/1/ina/6B_COMB.seq:*
55. /cgn2_6/ptodate/1/ina/PtoTUS_COMB.seq:*
67. /cgn2_6/ptodate/1/ina/PtoTUS_COMB.seq:*
67. /cgn2_6/ptodate/1/ina/Packfiles1.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-243-542-5
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US-08-243-542-5
US-08-243-542-7
US-08-243-542-7
US-08-243-542-7
US-08-243-542-6
US-08-243-542-6
US-08-243-542-6
US-08-243-542-6
US-08-243-542-8
US-08-243-7228-3
US-08-244-728-3
US-08-244-796-17
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US-08-216-276A-32

US-08-216-276A-30

US-08-216-276A-18

US-08-219-262B-11

US-09-031-655-11

PCT-US91-03056-16
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                                                                                                                                                                                                                                                                                                                                                                                                383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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ZIP: MILLING DATE: MILLINGH USA
COMPUTER READBALE FORM:
NEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IDM PC/XY/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/477,407
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: US 08/243,542
FILING DATE: 13 MAY-1994
APPLICATION NUMBER: US 5-57455
FILING DATE: 12 SEPTEMBER 1994
APPLICATION NUMBER: US 6-49904
FILING DATE: 12 SEPTEMBER 1994
APPLICATION NUMBER: US 6-49904
FILING DATE: 12 SPREMBER 1994
APPLICATION NUMBER: US 6-4904
FILING DATE: 22 APRIL 1994
APPLICATION NUMBER: US 6-4904
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 6-84470
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 6-84470
FILING DATE: 22 APRIL 1994
APPLICATION NUMBER: US APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NARAWUSA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: MCC PROTEINS AND DNAS
TITLE OF INVENTION: EMCODING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: Alamazoo
CITT: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Furuya Case 1313
                                                                       human fetal brain cDNA library
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: Sequence 5, Application US/08477407
: Patent No. 5631351
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REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: FUI
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LENGTH: 1464 base pairs
TYPE: nucleic acid
              Homo sapiens
                                                                                                                                                                   1..1464
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       ORGANISM: HOMO
IMMEDIATE SOURCE:
LIBRARY: human
FEATURE:
                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-243-542-5
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STRANDEDNESS:
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                                                                                                                            162 ctgcccccacggcagccctcagggcccgctggcccacctgccagcctggcccttttgc 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 acaaaccccaagtcctccttgccaggccttcaaccactatctcagtgcatggcttccat 401
Query Match , 6.0%; Score 36; DB 1; Length 7218; Best Local Similarity 3.8%; Pred. No. 0.12; Matches 9; Conservative 138; Mismatches 93; Indels
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ZIP: 4000B-1699

COMPOTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inches, 1.44 Mb storage
CONPUTER: 1BM PC/XT/AT COMPETIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
APPLICATION NUMBER: US/08/243,542
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: : EMI, MITSURU
TITLE OF INVENTION: MCC PROFEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Furuya Case 1313
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APPLICATION NUMBER: JP 5-136602
FILING DATE: J4 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: Z2 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: Z3 FEBRUARY 1994
APPLICATION NUMBER: JP 6-73328
FILING DATE: Z3 APRIL 1994
APPLICATION NUMBER: JF 6-84470
FILING DATE: Z2 APRIL 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-243-542-5
IS-08-243-52-5
; Sequence 5, Application US/08243542
; Patent No. 5552526
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 32549
REFERENCY/DOCKET NUMBER: 91549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAMURA, YUSUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
                                                               Matches
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1S-GB-243-542-7

1S-GB-243-542-7

1S-GB-243-104-8

1S-GB-
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                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
                                TYPE: nucleic acid
STANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: Homo saplens
              1464 base pairs
                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 1..1464
US-08-484-355-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.5%; Score 33; DB 1; Length 1464; Best Local Similarity 55.8%; Pred. No. 0.5; Matches 63; Conservative 0; Mismatches 50; Indels
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COUNTRY: MICHIGANING
COUNTRY: MICHIGANING
COMPUTER: BADABLE FORM:
MEDIUM TYRE: DISKETE, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT COMPAILD
OPERATING SYSTEM: MS-DOS 5.0
SOFWARE: MORPERE: US/08/484,355
FILING DATE: 07-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/243,542
FILING DATE: 11-MAY-1994
APPLICATION NUMBER: JP 5-136602
FILING DATE: 21 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 FEBRIARY 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APPRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 22 APPRIL 1994
APPLICATION NUMBER: 32 549
RECISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: FULUY GASE 1313
TELECOMUNICATION INFORMATION:
MARE: TETYMATION:
NAME: TETYMATION:
NAME: TETYMATION:
NAME: TETYMATION:
NAME: TETYMATION:
MARE: TETYMATION:
NAME: TETYMATION:
NAME: TETYMATION:
MARE: TETYMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
TITLE OF INVENTION: BUC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCESS:
CORRESSORDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
CITY: Michigan
TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
ORCANISM: Homo sapiens
IMMDIATE SOURCE:
LIBRARY: human fetal brain CDNA library
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Sequence 5, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
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TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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; LOCATION: 1..1464
US-08-477-407-5
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ABDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage COMPUTER: IBM PC/XT/AT COMPCTIBLE
COMPUTER: OF COMPCTIBLE
FILING DATE: 07-UNN-1995
FILING DATE: 13-MAY-1994
FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSE:
STREET: 2026 Rambling Road
CITY: Kalamazoo
CITY: Kalamazoo
CITY: Walamazoo
COUNTKY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: : EMI, MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
                                                  NAME: TETYPENCE F. Chapman REGISTRATION NUMBER: 32 549
REFERENCE/POCKET NUMBER: Evruy
TELECCHMUNICATION INFORMATION:
TELEPHONE: (616) 381-5465
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2913 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
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Sequence 7, Application US/08484355

Patent No. 570544

GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMI, MITSURU
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to MRNA ORIGINAL SOURCE: ORGANISM: Homo saplens
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2038..2913
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28..2037
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LOCATION:
FEATURE:
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LOCATION:
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; LOCATION:
US-08-477-407-7
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Best Local Similarity 55.8%; Pred. No. 0.73;
Matches 63; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: JULD RAMDLING ROAD
CITYETE MICHIGAN
CONTRY: GAR
ZIP: MICHIGAN
ZUP: HOUGH-1699
ZUP: HOUGH-1699
ZUP: HOUGH-1699
ZUP: HOUGH-1699
ZUP: HOUGH-1699
ZUP: HOUGH-1699
ZUPH-1699
COMPUTER: IBM PC/XY/AT COMPATIBLE
COMPUTER: WORTHER HOUGH/AT/AO/
SOFTHARE: WORTHERS: US/OB/477,407
FILING DATE: US/OB/477,407
FILING DATE: US/OB/43,542
FILING DATE: US/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AT/AD/OB/AD/OB/AD/OB/AD/OB/AT/AD/OB/AT/AD/OB/AD/OB/AD/O
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Fatent No. 5631351
GENERAL INFORMATION:
APPLICANT: NAKAWURA, YUSUKE
TITLE OF INVENTION: MCC PROTEINS AND DNAS
TITLE OF INVENTION: EMCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
                                                                                                                                                                                                                                                           LIBRARY: human fetal brain cDNA library
                                                                                                        linear
PE: CDNA to mRNA
SEQUENCE CHARACTERISTICS:
LENGTH: 2913 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                     MOLECULE TYPE: CDNA to mi
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INMEDIATE SOURCE:
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2038..2913
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28..2037
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LOCATION:
FEATURE:
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LOCATION:
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: LOCATION:
US-08-243-542-7
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US-08-477-407-7
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OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WORDPRECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,542
FILING DATE:
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MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-243-542-6
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APPLICANT: ENT, MITZURU
TITLE OF INVENTION: MCC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: FLYNN, THIEL, BOUTELL 6 TANIS P.C.
STRET: 2026 Rambling Road
CITY: Ralmanaco
STATE: Michigan
COMPUTE: Michigan
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT COMPATIBLE
APPLICATION NUMBER: JP 5-136602
FILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
FILING DATE: 2 SEPTEMBER 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 2 SEPTEMBER 1994
APPLICATION NUMBER: JP 6-49904
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 12 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: TEXTYPICE: JAPRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: TEXTYPICE: JP 3549
RESERVEK/DCOKET NUMBER: FULUYA CASE 1313
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-1156
TELEPHONE: (616) 381-156
TELEPHONE: (616) 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08243542; Patent No. 5552526; GENERAL INFORMATION:
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2038..2913
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; LOCATION:
US-08-484-355-7
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STREET: 2026 Rambling Road
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 5-136602
FILING DATE: 14 FMY 1993
APPLICATION NUMBER: JF 6-4904
FILING DATE: 22 SEPTEMBER 1993
APPLICATION NUMBER: JF 6-4904
FILING DATE: 13 FEBRIARY 1994
APPLICATION NUMBER: JF 6-7338
FILING DATE: 12 APRIL 1994
ATTOKNEY/AGENT INFORMATION:
NAME: FELYPRICE TO FILING DATE: 32 APRIL 1994
ATTOKNEY/AGENT INFORMATION:
NAME: FELYPRICE TO FILING TELYPRICE TO TELYPRICE TO THE TELYPHONE: (616) 381-1156
TELEPHONE: (616) 381-11
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Patent No. 5631351
GENERAL INCENATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: EMT, MITSURUE
APPLICANT: EMT, MITSURUE
TITLE OF INVENTION: BUCODING THE SAME
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES:
OUGRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL 6 TANIS P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
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Query Match 5.5%; Score 33; DB 1; Length 2923; Best Local Similarity 55.8%; Pred. No. 0.73; Matches 63; Conservative 0; Mismatches 50; Indels
APPLICANT: NAKANURA, YUSUKE
APPLICANT: BEN', MITSURU
TITLE OF INVENTION: MDC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
COMBESSEE: FLYNN, THIEL, BOUTELL & TANIS P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STREET: 2026 Rambling Road
CITY: A1amazoo
STREET: Michigan
COUNTRY: WISA
CITY: WASUMALE PORM:
HEDIOM TYPE: DISKETE, 3.5 inches, 1.44 Mb storage
COUNTRY: MADONIC SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DNAR: US 08/243.542
FILING DATE: 107-UN-1995
CLASSIFICATION NUMBER: US 08/243.542
FILING DATE: 12 SEPTEMBER 1993
APPLICATION NUMBER: UP 5-136602
FILING DATE: 21 SEPTEMBER 1993
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 APRTEMBER 1994
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 ARPHEMER 1994
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 ARPHEMER 1994
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 ARPHEMER 1994
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 ARPHEMER 1994
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 ARPHIL 1994
APPLICATION NUMBER: UP 6-49904
FILING DATE: 12 ARPHIL 1994
APPLICATION NUMBER: UP 6-49904
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION HYROMENATION:
THERMONICATION HYROMENATION:
THERMONICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
IMBDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: 3' UTR
LOCATION: 1600..2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
28..1599
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1..27
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FEATURE:
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                                             COUNTRY: USA

ZIP: 49008-1699

COMPUTER READABLE FORM:
MEDIDIN TYPE: Diskette, 3.5 inches, 1.44 Mb storage COMPUTER READABLE FORM:
MEDIDIN TYPE: Diskette, 3.5 inches, 1.44 Mb storage COMPUTER: BW PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,407
FILING DATE: 13-AXY-1994
FILING DATE: 13-AXY-1994
APPLICATION NUMBER: JF 5-136602
FILING DATE: 13-AXY-1994
APPLICATION NUMBER: JF 6-49904
FILING DATE: 12 SEPTEMBER 1993
APPLICATION NUMBER: JF 6-49904
FILING DATE: JZ FEBRUARY 1994
APPLICATION NUMBER: JF 6-49904
FILING DATE: JZ APRIL 1994
APPLICATION NUMBER: JF 6-49904
FILING DATE: JZ APRIL 1994
APPLICATION NUMBER: JF 6-49904
FILING DATE: JZ APRIL 1994
APPLICATION NUMBER: JF 6-68470
FILING DATE: JZ APRIL 1994
APPORNEY/ASHET INFORMATION:
REGISTRATION NUMBER: JF 6-68470
FILING DATE: JZ APRIL 1994
ATTORNEY/ASHET INFORMATION:
RESTRENCE/CARACTERISTICS:
LENGHH: DATE: JZ APRIL JS 5-5000
FILING DATE: JZ APRIL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: human fetal brain cDNA library
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; Patent No. 5705341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3' UTR
1600..2923
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28..1599
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1..27
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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; LOCATION:
US-08-477-407-6
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123 aggtaatcctgaaggcaatcacggaggtgaagggacagctgccccacggcagcctca 182
                                                       Sequence 8, Application US/08477407
SEQUENCE INVENTION: BMI, MITSURU
TITLE OF INVENTION: BMC PROTEINS AND DNAS
TITLE OF INVENTION: BMC PROTEIL & TANIS P.C.
STREET: 2026 Rambing Road
STREET: 2026 Rambing Road
STREET: 2026 Rambing Road
STREET: 2026 Rambing Road
COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

TIP: 4908-169
COMPUTER READABLE FORM:
MEDIUM TIPE: DISKETCH S. 35 Inches, 1.44 Mb Storage
COMPUTER READABLE FORM:
MEDIUM TIPE: DISKETCH S. 30

COMPUTER: USA

COMPUTER: USA

COMPUTER: USA

SETTION DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/243.542
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: US 07-313602
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: JP 6-49904
FILING DATE: 13-MAY 1993
APPLICATION NUMBER: JP 6-49904
FILING DATE: 12-MEDIUM SP 6-49904
APPLICATION NUMBER: JP 6-4990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: human fetal brain cDNA library
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 3' UTR
LOCATION: 2308..3183
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COCATION:
US-08-477-407-8
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183 gggcccgctggccccacctgccagccctggccctttgctaccagatccccgc 235
                                          272 AGGACCCCTTCCCCACCTCATTACCGGACCCCTCCCAGATCCCCTC 324
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                                                                                                                                                                                                                                              December 1. Sequence 8. Application US/08243542

| Patent No. 5552506
| GENERAL INFORMATION:
| APPLICANT: EMI, MITSURU
| TITLE OF INVENTION: MUC PROTEINS AND DNAS |
| TITLE OF INVENTION: MUC PROTEINS AND DNAS |
| TITLE OF INVENTION: MUC PROTEINS AND DNAS |
| TITLE OF INVENTION: MUC PROTEIL & TANIS P.C. |
| TITLE OF INVENTION: MUC PROTEIL & TANIS P.C. |
| TITLE OF INVENTION: MUC PROTEIL & TANIS P.C. |
| TITLE OF INVENTION: THIEL, BOUTELL & TANIS P.C. |
| STATE: Michigan |
| CONFORTRY: USA |
| CONFORTRY: USA |
| CONFORTRY: USA |
| CONFORTRY: ISH PC/XY/AT. Competible |
| CONFORTRY: ISH PC/XY/AT. Competible |
| CONFORTRY: NS-DOS 5.0 |
| SOFTWARE: MOTOPETECE 5.0 |
| CONFORTRY: WG-DOS 5.0 |

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APPLICATION NUMBER: JP 6-49904
FILING DATE: 23 SEPTEMBER 1994
APPLICATION NUMBER: JP 6-49904
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: JP 6-84470
FILING DATE: 12 APRIL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FELYENCE F. CHAPMER: 32 549
REGISTRATION NUMBER: 32 549
REFERENCE/COCKET NUMBER: 32 549
REFERENCE/COCKET NUMBER: 31 549
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION NUMBER: 31 546
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 Dasa pairs
TYPE: nucleic acid
STRANDEDNESS: double
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IMMEDIATE SOURCE:
LIBRARY: human fetal brain cONA library
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-136602
RILING DATE: 14 MAY 1993
APPLICATION NUMBER: JP 5-257455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
WOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: 3' UTR
LOCATION: 2308..3183
FEATURE:
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US-08-243-542-8
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING BONE
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: 18
CORRESPONDENCE ADDRESS: ADDRESSE: AND CA 4433
CITY: HOUSTON STREET: P.O. BOX 4433
CITY: HOUSTON STREET: P.O. BOX 4433
COUNTRY: United States of America
2 IP: 77210
COMPUTER RADABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/199,780
FILING DATE: TOWNENT T
                                                                                                                                                                                                                                                                                                                                                                       123 aggtaatcctgaaggcaatcacggaggtgaaggggacagctgccccacggcagccctca 182
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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 3183;
Pred. No. 0.77;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMICO09P--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9502251
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEY: 79-9024
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 373 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                             5.5%;
                                                                                                                                                                                                                                             Query Match 5.5' Best Local Similarity 55.8' Matches 63; Conservative
3' UTR
2308..3183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 1..3753
PCT-US95-02251-2
                                                                                                               1..2307
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
PCT-US95-02251-2/C
                                                            : FEATURE:
: NAME/KEY:
: LOCATION:
US-08-484-355-8
NAME/KEY:
LOCATION:
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                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 3183;
Pred. No. 0.77;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 1.5 inches, 1.44 Mb storage COMPUTER: IBM PC/AT/AT Compatible OPERATING SYSTEM: MS-TOS 5.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION INMBER: US/08/484,355
FILING DATE: U7-JUN-1995
CLASSIFICATION NUMBER: US/08/243,542
FILING DATE: U3-MAY-1994
APPLICATION NUMBER: US 08/243,542
FILING DATE: U3-MAY-1994
APPLICATION NUMBER: U5 5.7455
FILING DATE: U3 FEPTEMBER 1993
APPLICATION NUMBER: U5 6-49904
FILING DATE: U3 FEPTEMBER 1994
FILING DATE: U3 FEPTEMBER 1994
FILING DATE: U3 FEBTEMBER 1994
FILING DATE: U3 FEBTEMBER 1994
FILING DATE: U3 FEBTEMBER 1994
APPLICATION NUMBER: U5 64470
FILING DATE: U3 APRIL 1994
APPLICATION NUMBER: U5 644470
FILING DATE: U3 APRIL 1994
APPLICATION NUMBER: U5 644470
FILING DATE: U3 APRIL 1994
APPLICATION NUMBER: U5 644470
FILING DATE: U3 APRIL 1994
APPLICATION NUMBER: U5 644470
FILING DATE: U3 APRIL 1994
APPLICATION NUMBER: U5 644470
FILING DATE: U5 APRIL 1994
APPLICATION NUMBER: U5 644470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NKRAWURA, YUSUKE
APPLICANT: EMI, MISURU
TITLE OF INVENTION: MC PROTEINS AND DNAS
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
STRET: 2026 Rambling Road
CITY: Ralamazoo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08484355
Patent No. 5705341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32 549
REFERENCE/DOCKET NUMBER: Fu-
TELLECOMMUNICATION INFORMATION:
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TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 8:
                                                         Query Match
Best Local Similarity 55.8%;
Matches 63; Conservative (
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LENGTH: 3183 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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IMMEDIATE SOURCE:
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COUNTRY: USA
ZIP: 49008-1699
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MOLECULE TYPE: C
ORIGINAL SOURCE:
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Query Match

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Ouery Match 5.4%; Score 32.2; DB 5; Length 3753; Best Local Similarity 52.6%; Pred. No. 1.5; Matches 70; Conservative 0; Mismatches 63; Indels 0.
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APPLICANT: Yin, Wushan
TILLE OF INVENTION:
APPLICANT: Yin, Wushan
TILLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP)
TITLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP)
TITLE OF INVENTION: GENES, CONFOSITIONS AND METHODS
NUMBER OF SEGUENCES: 13
CORRESPONDENCE ADDRESS: 13
CORRESPONDENCE ADDRESS: 13
CORRESPONDENCE TO STATE: Texas
COUNTYTE: 104
COMPUTER: READABLE FORM:
MEDIU TYPE: PLOPPY disk
COMPUTER READABLE FORM:
MEDIU TYPE: PLOPPY disk
COMPUTER: BAPLICATION DATA:
APPLICATION NUMBER: US/OS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CLASSIFICATION DATA:
APPLICATION NUMBER: US/OS/MS-DOS
CLASSIFICATION NUMBER: US 08/199, 780
FILING DATE: 30-5EP-1994
APPLICATION NUMBER: US 08/199, 780
FILING DATE: 18-FEB-1994
ATTORNEY AGENT INFORMATION:
FELEPHONE: (713) 934-7001
INFORMATION FOR SEQ ID NO: 3:
SECOURCE CHARACTERISTICS:
LENGTH ADDRESS PAIRS
                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08479722B Patent No. 6074840
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STRANDEDNESS: single
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US-08-479-722B-3/c
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Eukaryota: Metazoa: Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae: Mus.

Eukaryota: Metheria: Rodentia: Sciurognathi; Muridae: Mus.

Eukaryota: Lo 935)

Eukaryota: Institutes of Health, Mammalian Gene Collection (MCC)

Institutes of Health, Mammalian Gene Collection (MCC)

Ontact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nth.gov

Contact: Robert Strausberg, Ph.D.

Contact: Mammalia Taker Mammalian (MCC)

Contact: Mammalia Taker Mammalia (MCC)

High quality sequence stort: 3

High quality sequence stort: 3

Location/Qualifices
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   cctgcagatatgcgcccagagatatggatcgcccaagagttgcggcgtatcggagacgag 474
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BG921698
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S Adachl.J., Alzawa.K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakwa.T. Baldarelli.R. Bono,H., Brownstein,M., Bult,C.
Carninci,P., Fikuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,R., Hiraoka,T., Hori,F., Hane,D., Imotani,K., Ishi,Y., Itch,M., Izawa,M., Kasukawa,T., Kawai,Y., Kojima,Y., Konno,U., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Sahito,M., Sakai,K., Sahinagawa,A., Shiraki,T., Sahito,H., Sahi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGAGAGGATCCAGGACTATTTTTTTTTTYN 3', CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 7.5 and subtraction to sequence [5' Grood strand cDNA was prepared with the primer adapter of sequence [5' DNA was prepared with the primer adapter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehlro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mali:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib-*RIKEN full-length enriched mouse cDNA library*/dev_srage-*10 days embryo*
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The RIKEN Genome Exploration Research Group Phase II Team and the FARTOM Consortium.
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/note="Boll-like 11 (apoptosis facilitator)
data source:NGD, source key:NGI:1197519, evidence:18S"
1 339 c 298 g 301 t. 3 others
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                                                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 1206)
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/strain="C57BL/6J"
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/db_xref="taxon:10090"
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1. 1206
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/organism="Homo sapiens"
/db.xref="taxon:9606"
/db.xref="taxon:9606"
/clone="IMAGE:2131313"
/clone_lib="NIB_MGC_118"
/tissue_type="leukocyte"
/lab_host="Pukla"
/note="vector: pcNv-SPORT6; Site_1: NotI; Site_2: EcoRv
/note="vector: pcNv-SPORT6; Site_1: NotI; Site_2: Note:
/note: pcNv-SPORT6; Site_1: NotE; Site
                                                     National institutes or Health, Mammalian Gene Collection (MCC)
Contact: Robert Strausberg, Ph.D.
Email: capaber refaal.inh.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:
http://mage.llnl.gov
Plate: LLAM1556 row: 1 column: 02
High quality sequence stop: 696
I. 700/Qualifiers
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            NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammallan Gene Collection (MGC)
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llarity 96.2%; Pred. No. 1.1e-91;
Conservative 0; Mismatches 9; Indels 8;
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es 433; Conserv
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/db_xref="taxon:10090"
/clone_lib="taxon:10090"
/clone_lib="taxon:10090"
/sex="female, virgin"
/sex="female, virgin
/sex="fema
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammallai, Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
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Pred. No. 2.9e-97;
0; Mismatches 61; Indels 24;
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ilarity 85.7%;
conservative
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/organism="Mus musculus"
/db_xref="taxon:10090"
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Euthorius

Rutaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Mus.inchamalia: Eutheria: Rodentia: Sciurognathi: Muridae; Mus.inchamalia: Eutheria: Rodentia: Sciurognathi: Muridae; Mus.inchamalia: Eutheria: Rodentia: Sciurognathi: Muridae; Musculus: Reman, M., Feldblyum, T., Malek, J., Shatsman, S., Akinret, A. B., Levins, M., Hogann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Context Gas RPCI-23-27793.TJ

Context Gas: RAPING Labo

Context: Shaying Labo

Department of Enkaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ndce-"Grgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
vith a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
162 c 138 g 142 t
                      AZ706148 580.bp DNA linear GSS 24-JAN-2001
RPCI-23-227P3.TV RPCI-23 Mus musculus genomic clone RPCI-23-227P3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhaoetigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). DAC end

page: http://www.tigr.org/fdb/bac_ends/mouse/bac_end_intro.html

Seg primer: 77
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/clone="RPCI-23-227P3"
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                                                                                                A2706148.1 GI:12433319
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                                                            DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E I (bases I to 645)

E Arakwa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Hatauyama, T., Miyazaki, A., Nomura, K., Ohno, M., Kouda, M., Koya, S., Hatauyama, T., Miyazaki, T., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Sano, H., Saski, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y. Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, E., Takeda, Y., Tanaka, T., Toya, T., Unpublished (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-25 Suchino-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB651225 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230069E03 5', mRNA sequence.
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URL:http://genome.gec.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Asyashizaki,Y.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
438 TGCCAGGCCTTCAACCACTATCTCAGTGCAATGGGT 473
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male testis"
/sex="male"
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                                                                                                                                                                                                                                                                             /clone_llb="RIKEN full-length enriched, 0 day neonate
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BB577135.2 GI:16449433
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Libraryciti, Restoro; Lockette, Carlucognath; Nuridee, Nurilecentum, Mammalia: Ethieria: Rodentia; Sciurognath; Nuridee, Nurilece, Nura. Arakwar, Carninci, P., Pukuda, S., Puruno, M., Hangashi, T., Blara, M., Libra, K. E., Libra, K. E., Libra, K. E., Libra, K. E., Libra, M. E., Monara, K., Ohno, H., Sasaki, D., Shinbata, M., Shinbata, M., Shaki, K., Shono, H., Sasaki, D., Shinbata, M., Shinb
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/organism-"Mus musculus"
                                                                                                                                        /strain="CD-1"
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transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to ROL = 5.0 and subtraction to ROL = 100.0. Second strand CDNA was prepared with the primer adapter of sequence [5 GAGAGGAGTACTGAGATAATAAATCACCCCCCCCCCCC 7]. CDNA was cloned into the Khol and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I. Cloning sites, 5' end: Sall; 3' end: BamHI."
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452 bp mRNA linear EST 29-DEC-2000 uy5909.yl McCarrey Eddy round spermatid Mus musculus cDNA clone un45909.sl sistematid for the cone clone and the cone muscal sistematid for the cone mediate to TR:054918 054918 BCL2 INTERACTING MEDIATOR OF CELL DEATH ;, mRNA sequence.
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Onderwood, K., Stepfoe, M., Theising, B., Allen, M., Bovers, Y., Person, B. Swaller, T., Glubons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washu-Nci Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l: mouseest@watson.wustl.edu clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 octgoggagagagoctcoccagctcagacctggggccctacctccctacagacagagcca 120
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                                                                                                                                                                                                                                                                        Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
1413 1314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                      Indels 12;
                                                                                                                                                                                                                                    Length 686;
                                                                                                                                                                                                                                  Score 328.4; DB 9;
Pred. No. 8.8e-83;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF021882.1 GI:10753214
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Best Local Similarity 91.7%;
Matches 363; Conservative
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AUTHORS
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BF021882
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/clssue_type="round spermatids, pooled from multiple mice"
/tissue_type="round spermatids, pooled from multiple mice"
/de_stage="60 day"
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/lab_host="01100 (phage-resistant)"
/lab_host="01100 (phage-resistant)"
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); Site_1: XhoII: Site_2: Econf: cDNA oligo dT-primed
); Site_1: XhoII: Site_2: Econf: cDNA oligo dT-primed
); Site_1: XhoII: Site_2: Econf: And Give_tone of the strange in Strange in Strange in Site_1: Site_2: Selection of the subtrange was mass excised (from lambda-uliang from 1-2 kb. Library was mass excised (from lambda-uliang tropped and tranformed into DH10B. Library contains SB.5% recombinants.

References: J. Androl. 20:635-639 and Gene 25:263-269. Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Blumedical Research, Dept. of Genetics): excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG173095 668 bp mRNA linear EST 06-FEB-2001 602336666F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4459720 5', mRNA sequence.
IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1424601
Seq primer: Primer name ambiguous
High quality sequence stop: 386.
Location/Qualifiers
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                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:3663833"
/clone_lib="McCarrey Eddy round spermatid"
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603170532F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:5250271 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
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/organism-"Mus musculus"
        227 9
                                                                                                                                                                                                          mRNA sequence.
BI454637
BI454637.1 GI:15245293
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Matches 250; Conservative
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235 c 162 g 136 t
                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi; Mammallai; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 668)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                 Email: gapbs remail.nlh.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayd by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov. c. column: 17
Plate: LLAH10260 row: c. column: 17
High quality sequence stop: 599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .668
/organism="Mus musculus"
/strain="FVB/N"
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 684)

1 (Dases 1 to 684)

2 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horl,F., 18hil,Y., 1to,M., Kawa,J., Konno,H., Kouda,M., Koya,S., Metayama,T., Miyazaki,A., Nomura,K., Ohno,M., Koya,S., Metayama,T., Miyazaki,A., Sakai,K., Sano,H., Sasaki, D., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,M., Takawa,A., Takakashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. et al. 2001)

N. Muramatsu,M. and Hayashizaki, et al. 2001)

Contect: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan Fai: 81-45-503-9216
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Y. and Hayashizaki, Y.

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(RE.http://genome.gsc.riken.go.jp,

Carninci.P., Shibata.Y., Hayatsu.M., Sugahara.Y., Shibata.K., Itoh

'M., Konno.H., Okazaki.Y., Muramatsu.M., and Hayashizaki.Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapped discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

wachiki.M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB653788 IXEN full-length enriched, adult male liver tumor Mus musculus cDNA clone C730026B05 5', mRNA sequence.
BB653788 I GI:16487616
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Hawamalia; Eutheria; Rodentia; Sciurognathi; Huridae; Hurinae; Hus.

Akumura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraokaj, T., Hirozane, T., Imotani, K.,
Hayatsu, N., Hiramoto, K., Hiraokaj, T., Konno, H., Kouda, M., Matsuyana, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinaqawa, A., Shiraki, T., Sogabo, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Hatahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Rike.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                  BB856627 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370035M16 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-45-503-9216
Email: genome-recequeriken.go.jp,
URL:http://genome-gasc.riken.go.jp,
Carninci.P., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh
WR.:http://genome.gasc.riken.go.jp,
M.: Konno,H., Okazaki.Y., Muxamatsu.N. and Hayashizzaki.Y.
Normalization and subtraction of cape-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new perpare full-length cDNA libraries for rapid discovery of new prepare full-length cDNA libraries for rapid discovery of new wagi.K., Fullwake,S., Inoue,K., Togawa,Y., Togawa,M., Ohara,E., Watahiki.M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,T., Marsuura S., Kawai.Y., Okazaki,Y., Muramatsu.N., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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175 c 121 g 96 t
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Pred. No. 4e-42;
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/strain="C57BL/6J"
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87.5%;
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Homo saptens

Eukaryota; Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 492)

S NCI-CAD http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

L Onpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue procurement; Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Preparation: M. A.G.E. Consortium/LLML at:

Www-blo.lini.gov/bbrp/image/Anage.html

Insert Length: 712 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence scop: 450.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-Torgan prostate; Vector: p773D-Pac (Pharmacia)
vith a modified polylinker; Plasanid DNA from the
normalized library NCLCGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The divier was PCR-amplified cDNAs from a pool
of 5.000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and 2 others
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2488679"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
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                                                                                                                                                                                                                                             'clone_lib "RIKEN full·length enriched, adult male liver
Hayashizaki,Y. Compared with Husan General Analysis of Full-Length Mouse cDNAs Compared with Human Genome 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                             /tissue_type="liver tumor"
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    .684
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    /db_xref-"taxon:10090"
    /clone-"C730026B05"

                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                         /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.1
Best Local Similarity 83.0
Matches 249; Conservative
                                                                                                             mouse tissues
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Length 620; Indels

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Query Match 18.9%; Score 112.8; DB 9;
Best Local Similarity 94.4%; Pred. No. 2.6e-21;
Matches 117; Conservative 0; Mismatches 7;
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiranoto, K., Horl, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Kawai, J., Konno, H., Koya, S., Matsuyama, T., Miyazaki, A., Ohno, M., Okazaki, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, M., Tagawa, A., Takahishi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. akeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. et al. 2001)

M. Unpublished (2001)

M. Gontect: Yoshinide Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., Thoustory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

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1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922.

Fax: 81-45-503-922.

Fax: 81-45-503-922.

Fax: 81-45-503-922.

M. Konno, H., Okazaki, Y., Hayatsu, N., Sugahara, Y., Shibata, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)

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Y. and Hayashizaki, Y.

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Kondo, S., Shinagawa, A., Saltor, T., Kiyosawa, H., Yamanaka, I., Alzawa L., Kiyosawa, H., Yamanaka, I., Alzawa L., Kiyokawa, H., Yamanaka, I., Alzawa L., Kiyokawa, H., Yamanaka, I., Alzawa L., Kiyokawa, H., Yamanaka, I., Alzawa L., K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for Lurther details.
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/clone='InDecender | Graph | Gra
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Eukeryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Bukryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Bukryota, Metazoa: Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 912)

National Institutes of Health, Nammalian Gene Collection (MCC)

National Institutes of Health, Nammalian Gene Collection (MCC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llni.gov
BI555336 912 bp mRNA linear EST 05-SEP-2001 603236095F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5289406 5',
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Location/Qualifiers
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BI555336.1 GI:15442650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Bukaryota: Eutherla: Primates: Catarrhini; Hominidae; Homo.

(bases 1 to 135)
Robertson, N.G., Khetarpal, U., Gutierrez-Eapeleta, G.A., Bieber, F.R.
and Morton, C.C.
Isolation of novel and known genes from a human fetal cochlear CDNA
library using subtractive hybridization and differential screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI497208 133e06.y1 Worton Fetal Cochlea Homo saplens cDNA clone IMAGE:2337938 5', mRNA sequence. BI497208 GI:15336552
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UNA sequencing and analyses were performed by National Institutes

ONA sequencing and analyses were performed by National Institutes

of Health Intramural Sequencing Center (NISC; see

http://www.nisc.nih.gov).

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@finage.llnl.gov) for further information.

Plate: LIAM6321 row: I column: 11

Seq primer: MI3RP1 reverse primer (ABI).
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! Continuation (3 of 5) of
! Continuation (4 of 5) of
! ACO26803 Homo saplens chr
! AP003936 Oryza sativa chr
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unidentified.

unidentified.

unidentified.

(Cases 1 to 596)

RS O'Reilly L., Puthalaketh, H., Adams, J., O'Connor, L., Cory, S., Huang, D.C. and Strasser. A.

Rovel therapeutic molecules

RD Appla21-A p 25-MAR-1999;

INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY LORRAINE O (AU); HUANG DAVID C S (AU); STRASSER ANDREAS (AU)

LOCATION/Qualifiers

1. .596

//OLAROILE LAXON: 32644*

//OLAROILE LAXON: 32644*

//OLAROILE LIONARE DAVID C S (AU); STRASSER ANDREAS (AU)

//OLAROILE LAXON: 32644*

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//OLAROILE LIONARE DAVIDENT REPORTER PROPERPROLER PROPERPORT PRANCE PROPER PROPERTINE PRANCE PROPERTICAL PROPE
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Gaps: 0
Percent Identity: 100.000
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   8.1e+03
1.0e+04
1.0e+04
2.1e+04
1.7e+04
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                                                                                                                                                                                                                                       Sequence 9 from Patent WO9914321.
AX031287
AX031287.1 GI:10278618
      92.99
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Ratio: 5.379
Percent Similarity: 100.000
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US-09-508-832-10 x AX031287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Len | Documentation | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1960 | 1
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AL607104 Oryza sativa chromo
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ACO2841 Homo sapiens chrome
ACO5095 Homo sapiens BAC Cl
ACO95292 Rattus norvegitus C
                                                                                                                                                                                                      -WOODEL-frame+_DA. model -DEV*xlh
-WOODEL-frame+_DA. model -DEV*xlh
-WOODEL-frame+_DA. model -DEV*xlh
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-DB-CGnbabl -OFWT-fastap -SUFFIX-rg- -GAPOP-12.000 -GAPOP-4.500
-HINNATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GAPOP-4.500
-FGAPEXT-1.000 -YGAPOP-10.000 -YGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -PLELOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -YAR_WIN-0
-ALIGN-15 -DOCALIGN-200 -THR_SCORE-PCT -THR_MAX-100 -THR_MIN-0
-ALIGN-15 -MODE-LCCAL -OUTFWT-PFF -NOME-ext -HBAPSIZE-500
-ALIGN-10 -MAXLEN-200000000 -USRR-USP9508812_ECGNL_1_3954
-NCPU-6 -ICPU-3 -LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30
                                                                                                         software, version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10570
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      out_format : pfs
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2 5 66-28
2 66-28
6 56-28
6 56-38
6 56-38
6 56-38
1 66-24
1 86-14
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2.0e+03
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1.2c+04
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1.1e+04
                                                                                                      About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199.10
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Query: Us 09-508 832-10
Query length: 198
Database: GenEmbl:*
Database sequences: 1797656
Database length: 1873333701
Search time (sec): 1829.680000
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                                                   Date: Aug 7, 2002 10:35
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gb_pr: AB071197
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9b_ro:AF0619556
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9b_pr:AR031285
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9b_pr:AR031381
9b_pr:AR031381
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9b_no.AX031305
9b_ro.AR032461
9b_ro.AR065432
9b_ro.AR065431
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seq_documentation_block:
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VERSION
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SOURCE
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JOURNAL
MEDLINE
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REFERENCE
AUTHORS
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JOURNAL
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AUTHORS
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                                                                                                                                      101
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AYYARRVFLNNYQAAEDHPRWVLLRLLRYIVRLWNRMH"
                                                                                                                                                                                                                                                                                                                                                                                                              UNA 20-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified.

SM unidentified
unclassified.

1 (bases 1 to 596)

S O'Reilly.L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser,A.

Novel therapeutic molecules
Novel therapeutic molecules
INST HEDICAL W & E HALL (AU) ; PUTHALAKATH HAMSA (AU) ; REILLY
LORRAINE (AU) ; ADAMS JERRY (AU) ; CONNOR LIAM O (AU) ; CORY
SUZANNE (AU) ; HUANG DAVID C S (AU) ; STRASSER ANDREAS (AU)
                                     GAAGATCCTCCTGCTGTCTCGATCCTCCAGTGGGTATTTCTCTTTTGAC 300
                                                                                                                                                  etArgGlnAlaGluProAlaAspNetArgProGluIleTrpIleAlaGln 150
                                                                                                                                                                   167 lPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetValileL 184
                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                            Length: 198
Gaps: 0
Identity: 100.000

    >594
    /note="unnamed protein product"

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/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AX031313
DEFINITION Sequence 9 from Patent WO9914321.
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AX031313.1 GI:10278641
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Ratio: 5.379
Percent Similarity: 100.000
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US-09-508-832-10 x AX031313
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
               251
                                        101
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PRI 19-FEB-1998
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1 (bases 1 to 597)
O'Connor,L., Strasser,A., O'Reillly,L.A., Hausmann,G., Adams,J.M., Cory,S. and Huang,D.C.
Bim: a novel mannag,D.C.
EMBO J. 17 (2), 384-395 (1998)
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O'Connor, L., Strasser, A., O'Reilly, L.A., Hausmann, G., Adams, J.M., O'Connor, L., Strasser, A., O'Reilly, L.A., Hausmann, G., Adams, J.M., Direct Submission
Submitted (03-NOV-1997) Molecular Genetics of Cancer, The Walter Eliza Hall Institute of Medical Research, PO Royal Melbourne
                                                                                                                                                                                                                                                  501 ATTITICAATAATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCT 550
                                                                                                                                                                                                                                                                                                                ThraspargSerProAlaProMetSerCysAspLysSerThrGlnThrPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArgVa 167
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                                                                                                                                                                                       oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA
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/note="alternatively spliced: see also Acc*
AB071195-AB071196, AB071198-AB071200*
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/db.xref="alm-bet
                                                                                                                                                                                     PRI 05-DEC-2001
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Submitted (06-SEP-2001) Toshiyuki Miyashita, National Children's
Wedical Research Center, Department of Genetics; 3-35-31 Taishido,
Setagaya, Tokyo 184-8809, Japan (E-mail:tunyashita@nch.go.jp,
Tel:81-3-3414-8121(ex.2763), Fax:81-3-3414-3208)
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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U.M., Miyashita, Frimates; Catarrhini; Hominidae; Homo.
U.M., Miyashita, T., Shikama, Y., Tadokoro, K. and Yamada, H.
Molecular cloning and characterization of six novel isoforms
human Bim, a member of the prospoptotic Bcl-2 family(1)
FEBS Lett. 509 (1), 135-141 (2001)
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                                                                                                                                                          seq_documentation_block:
LOCUS AB071197 630 bp mRNA linear
LOCUS AB071197 67 Bim-betal, complete cds.
ACCESSION AB071197.1 GI:17351900
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             Gaps: 1
Percent Identity: 94.737
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/db_xref="taxon:9606"
1. 408
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1. 408
/gene="bim-betal"
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Ratio: 5.301
nilerity: 94.737
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US-09-508-832-10 x AB071197
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                                                                                                           seq_name: gb_pr:AB071197
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Parkville, Victoria 3050, Australia Location/Qualifiers
1. 597
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1. 597
1. 597
1. 597

    1. .597
    /note-"pro-apoptotic BH3-containing

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Gaps: 0
Percent Identity: 100.000
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Ratio: 5.379
Percent Similarity: 100.000
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US-09-508-832-10 x AF032457
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51 ACAATTGCAGCCTGCGGAGAGGCCTCCCCAGCTCAGACCTGGGGCCCCTA 100
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Gaps: 2
Percent Identity: 82.083
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  AB071196-AB071200*
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a 190 c
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Ouality: 1010.50
Ratio: 5.104
Percent Similarity: 82.500
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US-09-508-832-10 x AB071195
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/note-"alternatively spliced: see also Acc
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                                                  201 TGCCAGCCCTGGCCCTTTTGCTACCAGATCCCCGCTTTTCATCTTTATGA 250
                                                                                                                                                                                                                                                              .......AlaSerMetArgGlnAlaGluPro 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 bp mRNA linear
Homo sapiens mRNA for Bim-alphal, complete cds.
AB071195
                                      OAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 510
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Miyashita,T.
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LOCUS AB071195
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/trānslation-"MAKOPSDVSSECDREGGGLQPAERPPOLRPCAPTSLQTEPOGNP
DGEODRCPHGSPGGPLAPPASPGPFATRSPLFIFVRRSSLLSRSSGYFSFDTDRSPA
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TTRYFFAUDYREAEDHPOWYLQLLRFIFRLVWRR"
178 C 150 9 125 t
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O'Rellly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,
Huang,D.C. and Strasser.A.
Huang,D.C. and Strasser.A.
Huang,D.C. and Strasser.A.
Huang,D.C. and Strasser.A.
Fatent: WO 9914321-A 25-MAR-1999;
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY
LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY
SUZANNE (AU); HIANG DAVID C S (AU); STRASSER ANDREAS (AU)
Location/Qualifiers
                                                                                                         1999 ACAGACAGGAGCCCGGCACCATGAGTTGTGACAAGTCAACACAAAACCCC 338
                                                                                                                                                 134 etArgGlnAla.....GluProAlaAspMetArgProGluIleTrpIle 148
                                                                                                                                                                                                                                                                           149 AlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaAr 165
                                                                                                                                                                                                                                                                                                                  165 gArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetV 182
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                                                                                            101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrPr
                                                                                                                                                                                                                      /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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/protein_id="CAC09660.1"
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/organism-"unidentified"
/db_xref="taxon:32644"
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AX031309
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LOCUS Ax031309
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                                                                                                                                                                          linear
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Gaps: 2
Percent Identity: 86.500
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                                                                                                                                                           seq_documentation_block:
LOCUS AX011283
AX011281
ACCESSION AX011283
ACCESSION AX011283
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1. .>587
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                                                                                                                                                                                                                AX031283.1 GI:10278614
                                                                              192 gLeuValTrpArgMetHis 198
                                                                                            701 CCTGGTGTGGAGAATGCAT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AX031283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908.00
4.935
92.000
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US-09-508-832-10 x AX031283
                                                                                                                                                                                                                                           unidentified.
unidentified
unclassified.
                                                                                                                                   seq_name: gb_pat:AX031283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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UNA 20-SEP-2000

linear

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Length: 200
Gaps: 2
Percent Identity: 86.500
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Thu Aug

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Percent Similarity:
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                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                    source
                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                          CDS
                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROD 19-FEB-1998
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Bim: a novel member of the Bcl-2 family that promotes apoptosis EMBO J. 17 (2), 384-395 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 591)
O'Connor,L., Strasser,A., O'Reilly,L.A., Hausmann,G., Adams,J.M.,
                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaClnCluLcuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaAr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etArgGlnAla.....GluProAlaAspMetArgProGluIleTrpIle 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                              OSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerM 134
                                                                                                                                                               63
                                                    1 MetalaLysGlnProSerAspValSerSerGluCysAspArgGluGlyAr 17
                                                                              1 ATGCCCAACCATCTGATGTAGTTCTGAGTGTGACAGAAGGTGG 50
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                                                                                                                                                                                                                                                                                                                                             GAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTATTTCTCTTTTTGAC
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                                                                                                                                                                                                                     GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr
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complete cds.
                           to: 590
                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AF032459
DEFINITION MUS MUSCULUS BIMEL MRNA,
ACCESSION AF032459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF032459.1 GI:2895499
                        to: AX031309
US-09-508-832-10 x AX031309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ro:AF032459
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                          Align seg 1/1
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VERSION
KEYWORDS
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JOURNAL
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AUTHORS
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                                                                                                          17
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/translation="MakOPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNP
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YTRYFANDYRRAEMOVILQLLFRIFRLVWRRH"
178 C 150 9 125 t
                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
1. 591
/note="pro-apoptotic BH3-containing Bcl-2 family member"
Cory, S. and Huang, D.C.S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 etArgGlnAla.....GluProAlaAspMetArgProGluIleTrpIle 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 200
Gaps: 2
Percent Identity: 86.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC40029.1"
/db_xref="GI:2895500"
                                                                                                                                                                                                                                                                                             /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="BimEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908.00
4.935
92.000
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US-09-508-832-10 x AF032459
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 591)
HSU.S.Y., Lin, P. and Hsueh, A.J.
BOD (BC1-2-related ovarian death gene) is an ovarian BH3
domain-containing proapoptotic BC1-2 protein capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::|||||||:::
611 TACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 etargGlnAla.....GluProAlaAspMetArgProGluIleTrpIle 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 gArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetV 182
                                                                                                                                                                                                                                                                                                      34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                                                                                                                    51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr 67
                                                                                                                                             1 MetAlaLysGlnProSerAspValSerSerGluCysAspArgGluGlyAr 17
        Percent Identity: 86.500
                                                                                                     to: 1137
                                                                                                       from: 1
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Rattus norvegicus
                                                                                                     Align seg 1/1 to: BC019556
        Percent Similarity: 92.000
                                          alignment_block:
US-09-508-832-10 x BC019556
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDMA Library Preparation: Life Technologies, Inc.
CON Sequencing by: Baylor College of Medicine Human Genome
Contect: Contect: Contect: Contect: Contect: Contect: Carcia, Mysc. Dom.tmc.edu
Contact: camgebcm.tmc.edu
Gunaratne, P.H., Carcia, A.M., Lu, X., Hulyk, S.M., Hale, S.M.,
Yoon, V.S., Kowis, C. R. Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MAKOPSDVSSECDREGGGLQPAERPPQLRPGAPTSLQTEPQGNP
DGEGDRCPHGSPGGPLAPPASPGPFATRSPLFIFVRRSSLLSRSSGYFSFDTDRSPA
PNSCDKSTQTPSPPCQAFNHYLSAMASIRQSGEEPEDLRPEIRIAQELRRIGDEFNET
                                                                                                                                                                                                   bcv19556 Has ausculus, BCL2-like 11 (apoptosis facilitator), clone MGC:28730 MAGE:4459720, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the L.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 37 Row: p Column: 14.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1137)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg,R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:10090"
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_the="McCGAP_Mam1"
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/note="Vector: pCNV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/protein_id="BCL2-like 11"
/db_xref="GI:18043533"
YTRRVEANDYREAEDHPOMVILQLLRFIFRLVWRRH*
330 c 282 g 250 t
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Gaps:
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4.935
                                                                                                                                                                                                 seq_documentation_block:
LOCUS BC019556
                                                                                                                                                          seq_name: gb_ro:BC019556
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Ratio:
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REYWORDS
SOURCE
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COMMENT
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PRI 05-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (06-SEP-2001) Toshiyuki Miyashita, National Children's
Submitted (06-SEP-2001) Toshiyuki Miyashita, National Children's
Medical Research Center, Department of Genetics; 3-35-31 Taishido,
Setagaya, Tokyo 154-8509, Japan (E-mail:tmiyashita@nch.go.jp,
Tel:81-3-3414-8121(ex.2763), Fax:81-3-3414-3208)
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             U.M., Miyashita,T., Shikama,Y., Tadokoro,K. and Yamada,M. Molocular cloning and characterization of six novel isoforms human Bin, a member of the proapoptotic Bcl-2 family(1) FEBS Lett. 509 (1), 135-141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="blm-beta2"
/note="alternatively spliced: see also Acc*
AB071195-AB071197, AB071199-AB071200"
                                                                       538
                                                                                                  AB071198 493 bp mRNA linear Homo saplens mRNA for Bim-beta2, complete eds. AB071198
                                       165 gArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetV
                                                         489 GAGGGCGTTTGCAAACGATACCGAGAGGCGGAAGACCACCCGCAAATGG
        439 GCACAGGAGCTGCGCGCATCGGAGCCAGTTCAATGAGACTTACACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 199
Gaps: 2
Percent Identity: 81.407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .408
                                                                                                                                                                                                                                                                                                Homo sapiens cDNA to mRNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"bim-beta2"
                                                                                                                                                                                                                                                                   AB071198.1 GI:17351902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 493)
Miyashita,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   837.50
5.138
81.910
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us-09-508-832-10 x AB071198
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                                                                                                                                                                                                     seq_documentation_block:
LOCUS AB071198
                                                                                                                                                                      seq_name: gb_pr:AB071198
                                                                                                                                                                                                                                                                                                                                                                  (sites)
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Ratio:
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                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
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VERSION
KEYWORDS
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TITLE
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TYRRAFANDYRAEABDHOMYLQLLRFIFRLVWRRH"
177 c 153 g 122 t
                                                                                                                                                                                                                                 ovarian death gene product BOD-L"
                                              flav. S.r. and Hsueh, A.J.W.

Hsu. S.r. and Hsueh, A.J.W.

Burect submission

Burect submission

Burect submission

Burect submission

Burect submission

Burect submission

Contino, Qualifiers

L. 391

/organism="Rattus norvegicus"

/organism="Rattus norvegicus"

1. 391

1. 391
dimerization with diverse antiapoptotic Bcl-2 members Nol. Endocrinol. 12 (9), 1432-1440 (1998) 98400436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1339 AAGTCCTCCTTGCCAGCCCTTCAACCATTATCTCAGTGCAATGCCTTCCA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGlnGluLcuargArgIleGlyAspGluPheAsnAlaTyrTyrAlaAr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 etArgGlnAla.....GluProAlaAspMetArgProGluIleTrpIle 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
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Percent Identity: 85.000
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                                                                                                                                                                                                                                                                                                                                                                                                                          693.00
4.880
91.500
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US-09-508-832-10 x AF065433
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Percent Similarity:
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84 251

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PAT 20-SEP-2000
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                                                                                                                                                                                                                                                                                               101 ThraspargSerProalaProMetSerCysaspLysSerThrGlnThrPr 117
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                                                                                                                                                                                                                                                                     from: 1 to: 181497
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Gaps: 0
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Location/Qualifiers
1. 181497
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a 40542 c 39097 g 49529 t
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DEFINITION Sequence 7 from Patent W09914321.
ACCESSION AX031285.
VERSION AX031285.1 GI:10278616
KEYWORSS.
ONGANISM unidentified.
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US-09-508-832-10 x AC096670/rev
                                                                                                                                                               Ouality: 713.00
Ratio: 5.443
Percent Similarity: 100.000
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unidentified
unclassified.
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   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 2 clone RPL1-438K19, complete sequence. AC096670 AC013332 AC096670.1 GI:15668150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (19-SRP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 19, 2001 this sequence version replaced 91:7248987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Nammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 181497)
Waterston, R.H.
The sequence of Homo sapiens clone (npublished)
2 (bases 1 to 181497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web' Site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Center project name: H_NH0438K19
Drafting center: WIBR
                                                                                                                                                                                                                                                                                              167
                                                                                     200
                                                                                                                                 134 MetArgGlnAlaGluProAlaAspMetArgProGluIleTrpIleAlaGl 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                           67
                                                       nGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArgV
                                                                                                                    oalaSerProGlyProPhealaThrArgSerProLeuPheIlePheMeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 LeuArgLeuLeuArgTyrIleValArgLeuValTrpArgMetHis 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTACGACTGTTACGTTACATTGTCCCCCTGGTGTGGGAGATGCAT 490
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397

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COMMENT

us-09-508-832-10.rge

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113 C 103 9
                                             UNA 20-SEP-2000
                                                                                                                                                               1 (bases 1 to 416)
O'Really, L., Puthalakath, H., Adams, J., O'Connor, L., Cory, S.,
O'Really, L., and Strasser, A.
Novel therapeutic molecules
Patent: NO 991431-A 25-MAR-1999;
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY
LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY
SUZANNE (AU); HANGO DAVID C S (AU); STRASSER ANDREAS (AU)
Location/Qualifiers
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Gaps: 1
Percent Identity: 69.697

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5.043
69.697
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US-09-508-832-10 x AX031311
                           seq_documentation_block:
LOCUS
AX031311
DEFINITION Sequence 7 fron
ACCESSION AX031311
VERSION
VERSION
X031311.1 GI
KEYMORS
ONGRE
ORGANISM unidentified
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unidentified
unclassified
 seq_name: gb_un:Ax031311
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113 c 103 9 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ...GACAGGAGCCCAGCACCCATGAGTTGTGACAAATCACAAACCC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etArgGlnAlaGluProAlaAspMetArgProGluIleTrpIleAlaGln 150
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                                                                                                                                                                                                                                                                                                                                                                                34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
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Percent Identity: 69.697

    >414
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 1. 416
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US-09-508-832-10 x AX031285
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124 ...GACAGGAGCCCAGCACCATGAGTTGTGAAATCAACACAAACCCC 170
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                                                                                                                   34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
 17 gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT
                                                                                                                                                                              51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr
                                                                                                                                                                                                           123 .....
                                                                                                                                                                                                                                      67 oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA
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Paphscorsorpcoperintlsaanswroaepabmrpeiwiaoelrrigdernay
Yarryelanyoaebhrwilkelkrivrlwrwh"
113 c 103 g
                                                                                                                                                                                                                                                                                                                                            PRI 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostoml; Mammalla; Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 417)
0 Connor.L., Strasser.A., O'Reilly,L.A., Hausmann,G., Adams,J.M., Cory,S. and Huang,D.C.
81m: a novel member of the Bcl-2 family that promotes apoptosis ENBO J. 17 (2), 384-395 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cory. S. and Huang, D.C.S.
Cory. S. and Huang, D.C.S.
Direct Submission
Submitted (03-NOV-1997) Molecular Genetics of Cancer. The Walter Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia

    417
    /note="pro-apoptotic BH3-containing Bc1-2 family member"
/codon_start=1

                                                      167 lPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetValIleL 184
                                                                                                                                                                                           linear
                                                                                                                                                                                                                                   69.697
                                                                                                                                                                                                                                                                                                                                    AF032458 ARNA, complete cds. AF032458
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Percent Identity:
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US-09-508-832-10 x AF032458
                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AF032458
                                                                                                                                                                                                                                                                                              seq_name: gb_pr:AF032458
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9430630
                                                                                                                                                                                                                                                                                                                                                                                                                      human.
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                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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465.15 563.98 126.75 137.91

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The present sequence encodes the extra long form (EL) of human Bim, or BCl-2 interacting mediator of cell death (see AAM98158), a novel corn BCl-2 interacting mediator of cell death (see AAM98158), a novel amenber of the BCl-2 family that is capable of inducing cell death appetosis) and which acts as a 'death-ligand' for certain members of the pro-survival BCl-2 family. Bim is a BH-3-only protein, as the only Bcl-2 homology region which it encompasses is BH-3. It is the only Bcl-2 homology region of a variety of isoforms, i.e. Bim-5. Bim-1 and Bim-EL. CDNAs encoding human Bim-1 and Bim-E. Sim-5. Bim-L and Bim-E. Sim-6. Bim-5. Bim-L and Bim-E. Isoforms (see AAW98158) were isolated from embryo and liver cDNA libraries using mouse bim cDNA. Murine Bim-5, Bim-L and Bim-E. Isoforms (see AAW98154-56) are also provided. The human Bim gene maps to chromosome 2 at bands 2q12-2q13. Binding the dynein light chain was shown to requilate the pro-apoptoric activity of Bim. Bim-5, the splice variant which does not bind to dynein light chain, is a much more potent killer than either Bim-1 or Bim-EL. The invention provides variant which does not bind to dynein light chain, is a much more potent killer than either Bim-1 or Bim-EL. The Lor Bim-EL that cannot bind, couple or otherwise associate with a dynein light chain. The identification and rational death, These Interapts of products for use in therapy, diagnosis, antibody generation and involving modulation as either antagonists or agonists of Bim's function and vill be useful in cancer, autoimmune or degenerative disease therapy. Increased Bim expression or Bim activity of Second deletion of autoreactive lymphocytes in autoimmune disease. Decreased Bim cancer and deletion of autoreactive lymphocytes in autoimmune disease.
     115.02
113.52
125.16
124.50
122.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
     seq_name: /SIDS1/9cgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX24997
                                                                                                                                                                                                                                                                                                                                                                                    Bim-EL; Bci-2 interacting mediator of cell death; apoptosis; cell cycle; human; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                                                                                                                                                                                                                                                            Human Bcl-2 interacting mediator of cell death Bim-EL cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated member of the Bcl-2 family, Bim used in, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Connor L, O'Reilly L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 101-102; 145pp; English
                                                                                                                                                                      62.98
62.98
62.98
103.16
157.90
157.90
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3.7e-51
1.7e-37
1.6e-30
4 1.6e-24
1.0e-18
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117.05
117.27
117.27
117.27
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177.99
179.26
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2.9e+03
99.51
5.4e+03
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146.58
200.86
228.56
393.32
                                                                                                                                                                        Sequence
Sequence
Signatory genescapt enemin/MA1999, DRT: MAXA997 + 1665.00 1205.199 2. 2ce-6
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 666.00 1068.41 3. 7ce-5
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 1068.41 3. 7ce-5
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 1068.41 3. 7ce-5
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 697.94 1. 6ce-
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 697.94 1. 6ce-
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 697.94 1. 6ce-
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 697.94 1. 6ce-
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA999 + 669.00 697.94 1. 6ce-
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA998 + 112.00 1255.74 117.
SIDDSI/grgdatary genescapt enemin/MA1999, DRT: MAXA99 + 112.00 1255.74 117.
SIDDSI/grgdatary genescapt enemin/MA1990, DRT: MA199 + 1112.00 1255.74 117.
SIDDSI/grgdatary genescapt enemin/MA1900, DRT: MA199 + 1112.00 1255.74 117.
SIDDSI/grgdatary genescapt enemin/MA1900, DRT: MA199 + 1112.00 1255.74 117.
SIDDSI/grgdatary genescapt enemin/MA1909, DRT: MA199 + 1112.00 1255.74 117.
SIDDSI/grgdatary genescapt enemin/MA1909, DRT: MA199 D
                                                                                        About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: US-09-508-832-10 to: N_Geneseq_032802:*
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Query: US-09-508-832-10
Query length: 198
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N

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expression of Blm activity is useful in regulating inhibition or prevention of cell death or degeneration such as under cytotoxic conditions during e.g. gamma-irradiation and chemotherapy or during HIVAIDS or other viral infections, ischemia, myocardial infarction, HIVAIDS or depenrative diseases or for prolonging the survival of cells being transplanted for treatment of disease. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity is useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lPheLeuAsnasnTyrGlnalaAlaGluAspHisProArgMetValIlet 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 ATTITIGAATAATTACCAAGCAGCCGAAGACCACCACGAATGGTTATCT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 oSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLeuArgArglleGlyAspGluPheAsnAlaTyrTyrAlaArgArgVa 167
                                                                                                                                                                                                                                                                                                                                                                                      oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA 84
                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaLysGlnProSerAspValSerSerGluCysAspArgGluGlyAr 17
                                                                                                                                                          Sequence 596 BP; 145 A; 175 C; 146 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euArgLeuLeuArgTyrIleValArgLeuValTrpArgMetHis 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1065.00 Length: 198
Ratio: 5.379 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-09-508-832-10 x AAX24997
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX24995

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ANX1995 standard; CDNA; 590 BP.

ANX1995 standard; CDNA; 590 BP.

ANX1995 standard; CDNA; 590 BP.

MAX1995 standard; CDNA; 590 BP.

MAX1995 standard; CDNA; 590 BP.

Murine Bel-2 interacting mediator of cell death Bin-EL CDNA.

Must bell-2 interacting mediator of cell death ben-EL CDNA.

Must bell-2 interacting mediator of cell death spotcasis;

ANA mass of the College mouse; cherapy; contraceptive; splice variant;

Must musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Must musculus.

Must musculus.

Muscu
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us-09-508-832-10.rng

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX24996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AlaGlnGluLeuArgArglleGlyAspGluPheAsnAlaTyrTyrAlaAr 165
                                                                                                                                                                                                                                                                                                        84 rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 etargGlnAla.....GluProAlaAspMetArgProGluIleTrpIle 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 GCACAGGAGCTGCGGCGGATCGGAGACGTTCAACGAAACTTACACAAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 gargValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Bc1-2 interacting mediator of cell death Bim-L cDNA.
                                                                                                                                                                                                                           34 hrSerLeuGlnThrGluProGlnGlyAsnProGluClyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                        17 gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 GAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTATTTCTCTTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 CAGGCTCTTTCCAAATGATTACCGCGAGGCTGAAGACCACCCTCAAATGG
                            Sequence 590 BP; 137 A; 178 C; 150 G; 125 T; 0 other;
                                                                                      Length: 200
Gaps: 2
Percent Identity: 86.500
                                                                                                                                                                                                to: 590
preventing generation of fertile sperm.
                                                                                                                                                                                              Align seg 1/1 to: AAX24995 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _documentation_block:
AAX24996 standard; cDNA; 416 BP.
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                                                                                      908.00
4.935
92.000
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US-09-508-832-10 x AAX24995
                                                                                                                   Percent Similarity:
                                                                                        Quality:
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                                                                          alignment_scores:
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The present sequence encodes the long form (L) of human Bin, or Bcl-2 interacting mediator of cell death (see AAM98157), a novel member of the Bcl-2 family that is capable of inducing cell death (apoptosis) and which acts as a death-ligand' for certain members of the pro-gurivial Bcl-2 family. Bin is a BH3-only protein, as the only Bcl-2 homology region which it encompasses is BH3. It is the only BH3-only protein for which splice variants exist. These conly BH3-only protein for which splice variants exist. These conly BH3-only protein for which splice variants exist. These heavy BH3-bin below the expression of a variety of isoforms, i.e. Bhn-5. Bin-L. and Bin-EL. cDMAs encoding human Bin-L and Bin-EL. Bhn-5. Bin-L and Bin-EL. cDMAs moroided. The human Bin gene maps to chromosome 2 at bands 2412-2431. Binding the dynain light channed as shown to regulate the pro-apoptotic activity of Bin. Bin-5, the splice variant which does not bind to dynein light channed by the splice variant which does not bind to dynein light conditions and which does not bind to dynein light condition and rational design of a range of products for use Interaction and rational design of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antagonists or agonists of Bin's function and will be useful in cancer, autoimmune or degeneration and involving modulation of therapy diagnosis, antibody generation and involving modulation of prevention of cell death. These therapeutic or prophylaxis in conditions such as cancer and deletion of prevention of cell death or degeneration such as under cytotoxic conditions during eq. gamma-liradiating bin expression of Bin activity is useful, in regulating the survival of configuration and challed of sterilization by provises of a generation of diseases. Since Bin is expressed in gene cells, modulating bin expression of bin activity is useful. Accounted the seases of contraceptine or a succes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment
               Bim-L; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle; human; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                                                                                                                                                                                                                                                                                              O'Reilly L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 416 BP; 113 A; 113 C; 103 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                              O'Connor L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 99-100; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Adams J, Cory S, Huang DCS,
Puthalakath H, Strasser A;
                                                                                                                                                                                                                                                                            97AU-0009373.
97AU-0009263.
                                                                                                                                                                                                                                      98WO-AU00772.
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW98157
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                                                                                                                                                       WO9914321-A1
                                                                                                                                                                                                                                      17-SEP-1998;
                                                                                                                                                                                                                                                                            24-SEP-1997;
17-SEP-1997;
                                                                              isoform: ss.
                                                                                                                                                                                             25-MAR-1999,
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W09914321-A1

us-09-508-832-10.rng

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Bim-L; Bcl-2 interacting mediator of cell death; apoptosis;
cell cycle; mouse; cancer; autoimmune disease;
degenerative disease; therapy; contraceptive; splice variant;
isoform; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GluLeuArgArglleGlyAspGluPheAsnAlaTyrTyrAlaArgArgVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine Bcl-2 interacting mediator of cell death Bim·L cDNA.
                                                                                                                                                                                                                                                                                                                                            101 CCTCCCTACAGACAGAGCCACAA.....123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 lPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetValIleL 184
                                                                                                                                                            34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                                                                                                                  51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr 67
                                                                                                                                     1 MetAlaLysGlnProSerAspValSerSerGluCysAspArgGluGlyAr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA 84
                                                                                                                                                                                                                                                                                                                                                                                                                          123 .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 euArgLeuLeuArgTyrIleValArgLeuValTrpArgMetHis 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 69.697
                                                                                                  to: 416
                                                                                               Align seg 1/1 to: AXX24996 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAX24994 standard; cDNA; 422 BP.
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                                     alignment_block:
US-09-508-832-10 x AAX24996
Percent Similarity: 69.697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX24994;
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The present sequence encodes the long form (L) of murine Bim, or Rel-2 interacting mediator of cell death (see AAW98155), a novel member of the Bol-2 family that is capable of inducing cell death (capabotosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bol-2 family. Bim is a BH3-only protein, as the conly Bcl-2 homology region which it encompasses is BH3. It is the conly Bcl-2 homology region which it encompasses is BH3. It is the conly Bill-only protein for which it encompasses is BH3. These conly BH3-only protein for which splice variants exist. These conly BH3-only protein for which splice variants exist. These conly BH3-only protein for which splice variants exist. These bim-E. (see AAW98164-56). CDNAs encoding these murine Bim combinant Bol-2 protein. The murine Blm gene has been mapped to chromosome 2 at bands from a T lymphoma cDNA library using human recombinant Bol-2 protein. The murine Blm gene has been mapped to chromosome 2 at bands from a T lymphoma cDNA library using human recombinant Bol-2 protein. The murine Blm-E. Bindon and solve the pro-apoptoric activity of Blm.

Chain was shown to regulate the pro-apoptoric activity of Blm.

Chain, is a much more potent Killer than either Blm-E.

Chain, is a much more potent Killer than either Blm-E.

Chain, is a much more potent Killer than either Blm-E.

Chain, is a much more potent Killer than of Mynein light chain. The daentification of Blm permits the chain. The daentification and rational design of a range of products for use with a dynein light chain. The deentification and will be complying a sell and activity is useful, e.g. for Increased Blm expression or Bim activity is useful in regulating inhibition or prevention of cell death. Or degenerative disease therapy or conditions during e.g. gamma-irradiation and chemotherapy in prophylaxis of Blm activity is useful in regulating inhibition of surpersion of Blm activity is useful in regulating being transplanted for treatment of prophylaxis, degenerative diseases. Since
                                                                                                                                                                                                                                                                                                                                                                    New isolated member of the Bcl-2 family, Bim used in, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm.
                                                                                                                                                                                                                                      Adams J, Cory S, Huang DCS, O'Connor L, O'Reilly L;
Puthalakath H, Strasser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 422 BP; 112 A; 116 C; 109 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 200
Gaps: 2
Percent Identity: 60.000
                                                                                                                                                                                             (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 94-95; 145pp; English.
                                                                                  98WO-AU00772.
                                                                                                                           97AU-0009373.
97AU-0009263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589.00
4.566
64.500
                                                                                                                                                                                                                                                                                                          WPI; 1999-244030/20.
                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW98155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                 17-SEP-1997;
                                                                                  17-SEP-1998;
                                                                                                                           24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                      25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                 treatment
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1 MetalaLysGlnProSerAspValSerSerGluCysAspArgGluGlyAr 17

to: 422

Align seg 1/1 to: AAX24994 from: 1

Mus musculus

X S X & & & & & & A X Y X P X

alignment_block: US-09-508-832-10 x AAX24994

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX24993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT: AAS65350
                                                                                                                                                                                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                             AlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaAr 165
                                                                                                                                                                                                                                                                                                                                        182 allleLeuArgLeuLeuArgTyrIleValArgLeuValTrpArgMetHis 198
                    123
                                                                                                  rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                               67
34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                67 oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA 84
                                                                                                                                                                                                                                                                                    51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #1154.
                                                                                                                                                                                                                                                                                                                                                                                     seg_documentation_block:
ID AAS65350 standard; cDNA; 442 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001
                                                                                                  123
                                                                                                                                               84
                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                          271
                                                                                                                                123
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and for exection (PCR) primers, collagmers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) as useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assessibildiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Conding sequence data for this patent did not appear in the printed septimical confine and the printed sequence the sequence of the confine paper.
                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 hrserLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 92
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 442 BP; 94 A; 154 C; 105 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 442
                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 1154; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATCCTCCCTGCTGTCTCGATCC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rgArgSerSerLeuLeuSerArgSer 92
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAS65350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 497.00
Ratio: 5.402
Percent Similarity: 100.000
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US-09-508-832-10 x AAS65350
                                                     WPI; 2001-639362/73.
P-PSDB; ABG01163.
Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
RT,
Drmanac
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The present sequence encodes the short form ($) of murino Bin, or Bcl-2 interacting mediator of cell death (see AAM98154), a novel member of the Bcl-2 family that is capable of inducting cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bcl-2 family. Bim is a BH3-only protein, as the only BH3-only protein for which splice variants exist. These only BH3-only protein for which splice variants exist. These conly BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. Bim-5, Bin-1 bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated member of the Bcl-2 family, Bim used in, e.g. cancer
                                                                                                                                                                                                   Bim-S; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                                                                                                            Murine Bcl-2 interacting mediator of cell death Bim-S cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams J, Cory S, Huang DCS, O'Connor L, O'Reilly L; Puthalakath H, Strasser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 92; 145pp; English.
                           8
seq_documentation_block:
ID AAX24993 standard; cDNA; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97AU-0009373.
97AU-0009263.
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-244030/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW98154
                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-1997;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                W09914321-A1
                                                                                                               05-JUL-1999
                                                                                                                                                                                                                                                                              isoform; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment
                                                                  AAX24993;
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is useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ACAATTGCAGCCTGCTGAGAGGCCTCCCCAGCTCAGGCCTGGGGCCCCTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 rgArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 etArgGlnAla.....GluProAlaAspMetArgProGluIleTrp11e 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMetV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 TTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 oSerProProCysClnAlaPheAsnHisTyrLeuSerAlaMetAlaSerM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                              34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                                 1 MctalaLysGlnProScrAspValScrScrGluCysAspArgGluGlyAr 17
                                                                                                                                                                                                                                                                                                                                   1 ATGCCCAAGCAACCTTCTGATGTAGTTCTGAGTGTGACAGAGGTGG 50
                                                                                                                                                                                                                                                                                                                                                                        17 gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 oAlaSerProGlyProPheAlaThrArgSerProLeuPhellePheMetA
                                                                                                                                                   vaps: 2
Percent Identity: 45.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 .....
                                                     Sequence 332 BP; 87 A; 85 C; 91 G; 69 T; 0 other;
                                                                                                                             Length:
                                                                                                                                                                                                                                                              to: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 CCFCCCTACAGACCGCAA......
                                                                                                                                                                                                                                                              Align seg 1/1 to: AAX24993 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAI89284 standard; cDNA; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001 (first entry)
                                                                                                                                                 4.101
                                                                                                                                                                                                      alignment_block:
US-09-508-832-10 x AAX24993
                                                                                                                               406.00
                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                            alignment_scores:
Quality:
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ប្បប្បវន្ត
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us-09-508-832-10.rng

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferention or cell differentiation or which may induce production of other cytokines in other cell populations. The peptide therapy, The polypetides are useful in gene therapy, vaccines or peptide therapy. The polypetides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or treatment be cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemla; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV35620
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 9344; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 23
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 371 BP; 106 A; 95 C; 81 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
Human polynucleotide SEQ ID NO 9344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AA189284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAV35620 standard; DNA; 32367 BP.
                                                                                                                                                                                                                                                           Drmanac RT;
                                                                                                                                                                26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-508-832-10 x AAI89284/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 gLeuValTrpArgMetH1s 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 CCTGGTGTGGAGAATGCAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 5.348
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 123.00
                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56.
                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                          Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                 P-PSDB; AAO09353
                                                                                                              WO200164835-A2.
                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                        07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV35620;
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This is the human SHOX gene sequence containing the PARI region. The gene region or corresponding to short stature has been identified as a region of approximately 500 kb in the PARI region of the x and Y chromosomes. Three genes in this region have been identified as a chromosomes. Three genes in this region have been identified as candidates for the short stature gene. These genes in the short stature gene. These genes were designated SHOX candidates for the short stature gene. The SHOX gene has two separate splicing sites resulting in two variations SHOX gene has two separate splicing sites resulting in two variations SHOX gene has two separate splicing sites resulting in two variations SHOX gene has SHOX separate so through sequences of SHOX (short stature homeobox containing) genes as SHOX ET92, SHOXA, SHOX, SHOX and exons of the SHOX genes as shown in AAV15610 to AAV1562 and protein sequences of the human growth protein transcription factor SHOXA, SHOXD and SHOT as shown AAW60573 to AAW60575. The movel genes are responsible for human growth. Defects in the genes can cause chort stature, e.g. Turner's syndrome. The products can be used to develop agents for the treatment of short stature or other human growth disorders. The products can also be used for providing a mitogenic effect on cells, e.g. for the treatment of bone diseases such as osteoporosis and diseases involved with disturbance in the bone calcium regulation.
                                                                     Homeobox domain; human growth gene; growth regulation; growth defect;
turner's syndrome; short stature homeobox containing gene; SHOXa;
SHOX; bone disease; osteoporosis; calcium regulation; short stature;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human growth genes - used to develop products for the diagnosis and treatment of human growth defects such as short stature, e.g.
Human SHOX (short stature homeobox containing gene) gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32367 BP; 7627 A; 8130 C; 8564 G; 8043 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 SerSerGluCysAspArgGluGlyArg.....GlnLeuGlnProAlaGl
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Gaps: 13
Percent Identity: 33.898
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96US-0027633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RAPP/) RAPPOLD-HOERBRAND G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rao E, Rappold-hoerbrand G;
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US-09-508-832-10 x AAV35620/rev
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Ratio: 1.271
Percent Similarity: 53.107
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                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-1997;
01-OCT-1996;
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us-09-508-832-10.rng

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/*cag= b
/note= "This deletion replaces Arg with Ile and results
in a premature stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dog: X-linked progressive retinal atrophy 1; XLPRA1; genetic marker; retinitis pigmentosa GTPase regulator; RPGR; Siborian Husky; Samoyed; Miniature Schnauzer; mutant; mutein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine retinitis pigmentosa GTPase regulator (RPGR) mutant #1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn·emb1/NA2001A.DAT:AAD07131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product "Canine retinitis pigmentosa GTPase regulator mutant" /note- "CDS does not include start codon"
                                                                                                                                                                                                                      13894 CAAGGCTCTCCCCAGGACACCAGGTCCCCAGGTCACCAG 13845
                 13994 TCCCGGGACACCAGGTCCCCAAGCCTCTCCCGGGTCACTAGGTCCCCAAG 13945
                                                                                                                                                         13794 CCAGGTGTTCAAGCCTCTCCGGGACACCAAGTCCCCAAGCC...... 13753
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13752 .TCTCCCGGGACACCAGGTCCCCAAGCCTCTCCCGGCTCACCAGATCTCC 13704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13703 AAGCCTCTCCCAGGACACCAGGTCCCCAAGCCTCTCCCAGGACACCAGGT 13654
                                                                                                                                                                                                                                                                                                                                        101 hr.....AspArg.SerProAlaProMetSerCysAspLy 112
                                                                                                                                                                                                                                                                                                                                                                                                             112 sSerThrGlnThrPro.....SerProProCysG 122
                                                                                                                                                                                                                                                                          85 gSerSerLeuLeuSerArg...SerSerSerGlyTyrPheSerPheAspT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 InalaPheAsnHisTyrLeuSerAlaMetAlaSerMetArg......135
                                                                                                                                   58 lySerProGln.....GlyProLeuAlaProProAlaSerProGlyPro 72
                                                                    58
                                                                                                                                                                                                         82
37 ln...Thr.GluProGlnGlyAsnProGlu.....
                                                                    46 .........GlyAsnHisGlyGlyGluGlyAspSerCysProHisG
                                                                                                                                                                                                     73 PheAla.....ThrArgSerProLeuPheIlePheMetArgAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13653 CCCCAAGCCTCTCCCCAGGACACCAGG 13627
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ID AAD07131 standard; cDNA; 2800 BP.
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The invention relates to a method for identifying dogs which are genetically normal, are carriers of, or are affected with X-linked progressive retinal atrophy (XLPRA), by testing a biological sample with progressive retinal atrophy (XLPRA), by testing a biological sample with genetic markers that co-segregate with a XLPRA gene locus. The invention also relates to canine retinitis pigmentosa GTPase regulator (RRGR), RPGR mutants and their corresponding nucleic acid molecules. The mutated RPGR genes are responsible for the XLPRA in dogs. Methods are used to select dogs for breeding so that dogs carrying the mutated locus are aliminated from the breeding stock. The method particularly applies to Siberian Husky, Samoyeds and Miniature Schnauzer breeds, or any other breed where the disease is X-linked. XLPRA1 type is identified in Siberian Huskles, and Samoyeds, while XLPRA2 type is identified in Miniature Schnauzers. The present cDNA sequence is the mutant open reading frame (ORF) 15 encoding Cannier retilities bygmentosa eggulator (RRGR) mutant in XLPRA1-affected dogs. This mutant is obtained by deleting 'GAGAA' mucleotide bases from position 878 to 882 of the wild-type
                                                                                                                                                                Identifying dogs with or carrying X-linked progressive retinal atrophy by detecting retinitis pigmentosa GTPase regulator gene mutation, useful when breeding Husky, Samoyed and Miniature Schnauzer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 CCTTCTTCCACTTCCTCCTCCTCCTCCTCCACTTCCCCTTCTCTTC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGlnPr 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ....SerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2800 DP; 1026 A; 287 C; 938 G; 549 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 oAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 hrGluProGlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSer
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                                                            zeiss CJ;
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Gaps: 6
Percent Identity: 27.517
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                                                            Ray
                                                                                                                                                                                                                                                       Claim 73; Page 32-33; 88pp; English.
                                                          Aguirre GD, Acland GM, Zhang O,
              (CORR ) CORNELL RES FOUND INC.
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US-09-508-832-10 x AAD07131/rev
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1.314
57.718
                                                                                                   WPI: 2001-367707/38
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found in XLPRA2-affected dogs. This mutant is obtained by deleting 'GA' nucleotide bases from position 932 to 933 of the wild-type canine RPGR cDNA.
                                                                Seguence 2803 BP; 1028 A; 287 C; 939 G; 549 T; 0 other;
                                                                                                                                                                                                  alignment_block:
US-09-508-832-10 x AAD07132/rev
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1.314
57.718
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Percent Similarity:
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     SSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying dogs with or carrying X-linked progressive retinal atrophy by detecting retinities pigmentosa Gyrasa requilator gene mutation, useful when breeding Husky, Samoyed and Miniature Schnauzer
                                                                                                                                                                                                                                                                                                            Dog; X-linked progressive retinal atrophy 2; XLPRA2; genetic marker; retinitis pigmentosa GTPase regulator; RPGR; Siberian Husky; Samoyed; Miniature Schnauzer; mutant; muteln; ss.
                                                                                                                                                                                                                                                                                 Canine retinitis pigmentosa GTPase regulator (RPGR) mutant #2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a /product- "Canine retinitis pigmentosa GTPase /product- "Canine retinitis pigmentosa GTPase /note= "CDS does not include start codon" replace (931...932, AGAG) /*tag= b //tote= "This deletion results in the change of amino acids and ends in a premature stop codon"
                                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD07132
125 snHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAla 140
                                                                                             Zeiss CJ;
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                                                                                                                                                             seq_documentation_block:
ID AAD07132 standard; cDNA; 2803 BP.
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P-PSDB; AAE02399.
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                                                                                                                                                                                                               AAD07132;
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation
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Dog; X-linked progressive retinal atrophy; XLPRA; genetic marker; retinitis pigmentosa GTPase regulator; RPGR; Siberian Husky; Samoyed; Miniature Schnauzer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD07130
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                                                                                                                                                                                                                                                                                                                                                                                    38 hrGluProGlnGlyAsnProGluGlyAsnHisGlyGluGlyAspSer 54
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                                                                                                                                                                                                         5 ProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGlnPr 21
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                                                                                                                                                                                                                                                                                             21 oAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnT
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Length: 149
Gaps: 6
Percent Identity: 27.517
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AAD07130 standard; cDNA; 2805 BP.
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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for petecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/nA2001A.DAT:AAL24943
                                                                      ......ProAlaProMetSe 109
                                                                                                                                                                                                                                109 rCysAspLysSerThrGlnThrPro...SerProProCysGlnAlaPheA 125
                                                                                                                                                                                                                                                              453 TCCTTCCTCCTCTCCCCTCTCCTCCCTCCTTGCTCTTGTT 404
                                                  84 rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                     125 snHisTyrLeuSeralaMetAlaSerMetArgGlnAlaGluProAla 140
                                                                                                                                                                                                                                                                                                                                                   Sequence 766 BP; 142 A; 127 C; 224 G; 273 T; 0 other;
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Gaps: 11
Percent Identity: 29.412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lillie J, Xu Y, Wang Y, Steinmann K;
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ID AAL24943 standard; cDNA; 766 BP.
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24-MAR-2000; 2000US-019099.
29-MAR-2000; 2000US-020530.
09-JUN-2000; 2000US-0205310.
25-JUL-2000; 2000US-020534.
                                                                                                                                       101 ThrAspArgSer.....
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1.600
45.752
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Quality:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL24943;
                                                                                             545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for identifying dogs which are genetically normal, are carriers of, or are affected with X-linked progressive retinal atrophy (XLPRA), by testing a biological sample with progressive retinal atrophy (XLPRA), by testing a biological sample with genetic markers that co-segregate with a XLPRA gene locus. The invention also relates to canine retinitis pigmentosa CTPsase regulator (RPGR), RPGR mutants and their corresponding nucleic acid molecules. The mutated RPGR genes are responsible for the XLPRA in dogs. Methods are used to select dogs for breeding so that dogs carrying the mutated locus are eliminated from the breeding stock. The method particularly applies to Siberian Husky, Samoyed and Miniature Schnauzer breeds, or any other breed where the disease is X-linked. XLPRA! type is identified in Miniature Schnauzers. The present CDNA sequence is the normal open reading frame (ORF) 15:

The present CDNA sequence is the normal open reading frame (ORF) 15:

Cound in normal dogs.
/product= "Canine retinitis pigmentosa GTPase regulator"
/note= "CDS does not include start codon"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying dogs with or carrying X-linked progressive retinal atrophy by detecting retinitis pigmentosa GTPase regulator gene mutation, useful when breeding Husky, Samoyed and Miniature Schnauzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 TCCCCCTCCAATTCCCCCTCTTTCTTCCCCTTTTCCCTCTCTCTC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 CICCACTICCCCCTICCTICCATTCTCCCCTCCTTCCTCCTCCAG 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 oAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 CysProHisGlySerPro.....GlnGlyProLeuAlaProProAla.. 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....SerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670 ccrcccrrrcrcrcrcrcrrrccrcrcrcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2805 BP; 1029 A; 287 C; 940 G; 549 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGlnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 hrGluProGlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AAD07130 from: 1 to: 2805
                                                                                                                                                                                                                                                                                                                                              Zeiss CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 149
Gaps: 6
Percent Identity: 27.517
                                                                                                                                                                                                                                                                                                                                              Ray K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 71; Page 30-31; 88pp; English.
                                                                                                                                                                                                                                                                                                                                            Aguirre GD, Acland GM, Zhang Q,
                                                                                                                                                                                                                                                                                                 (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                         2000WO-US31940.
                                                                                                                                                                                                                                                    99US-0167365.
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US-09-508-832-10 x AAD07130/rev
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Ratio: 1.314
nilarity: 57.718
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Percent Similarity:
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                                                                                                                 WO200138578-A1
                                                                                                                                                                                                         21-NOV-2000;
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                                                                                                                                                              31-MAY-2001
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA20018.DAT:AAS84424
                                                                                                                                                                                                                                                                                          94 SerGlyTyrPheSerPheAspThrAspArgSerProAlaProMetSerCy 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: (11] ::: (11] ::: (11] ::: (12] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] :: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] :: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (13] ::: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 CCATCCAGACGCATGCAAACCCCCAGACCCAGTCCCCATTCACCTACCAC 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 ACAGGCAAA.....GACACAGACCCAGACCCAGACCCAATC..... 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 yrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArg 143
                                                                                                                                                                                                        559 GGGAAAAGGAAGGGGCGGTAAATTCTTACATACCCCCCGAGCTTTGTGAT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 GCCCA.....CATTCAGACATACCCAAACATAGACAG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 sAspLysSerThrGlnThrProSerProProCysGlnAlaPheAsnHisT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                          52 lyAspSer.....CysPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 HisGly..... SerProGlnGlyPro.... 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ......LeuAlaProProAlaSerProGlyProPheAlaThrArgS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 erProLeuPheIlePheMetArgArgSerSerLeuLeuSerArgSerSer 93
                                                                                                                                                                        21 ProAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGl 37
                                                                                                              Align seg 1/1 to reverse of: AAL24943 from: 1 to: 766
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ID AAS84424 standard; cDNA; 2370 BP.
                    alignment_block:
US-09-508-832-10 x AAL24943/rev
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 AACCCAGAG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
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The Invention relates to isolated polynucleotide (I) and polyneptide (II) sequences. (I) is useful as hybridisation probes, polynerase chair reaction (PCR) primars, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) as useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for generic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on bin and amino acid sequences. Assetist-Assets and expense of the invention.

Claignostic coding sequences of the invention: appear in the printed security of the sequence data for this patent did not appear in the printed security from WIPO
                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1856 CT...... 1855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 Thr.AspargSerProAlaProMetSerCysAspLysSerThrGln...T 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819 TECTTCCCAGCCCATCTGGTCTCCACTGTGGCCCCTG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1782 Gerecegeereceacegeacagecegege......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2370 BP; 474 A; 623 C; 753 G; 520 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AAS84424 from: 1 to: 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112.00 Length: 129
1.836 Gaps: 7
47.287 Percent Identity: 31.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 20228; 103pp; English.
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-508-832-10 x AAS84424/rev
    Drmanac RT, Liu C,
                                                                       WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouality:
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Percent Similarity:
                                                                                                            P-PSDB; ABG20237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 31-40. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying blological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce microbial metabolites. The BLM gene cluster may also be used to produce
                    P-PSDB: AAB07580, AAB07581, AAB07582, AAB07583, AAB07584, AAB07585,
AAB07586, AAB07587, AAB07588, AAB07589
                                                                                New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6552 GAAGGCGTCAGGGACGGTCTCCGCCCCGGGCGCGGGCAGGTACCGCGGGC 6503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6752 GCCCCCAGGACGCCAGGAGGCCACGACGCCGTCGGCGGGGGCGCGCAG 6703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18660 BP; 2365 A; 7239 C; 6510 G; 2546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6652 CGGCCAGGCGGTGACCCGGGTGTCCAGCTCGGCGAACGTCAGCGTCGAG 6603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 etSerCyaAspLysSerThrGlnThrProSerProProCysGlnAlaPhe 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAs 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 OProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluProGlnG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 lyAsnProGlu.....GlyAsn 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisGlyGlyGluGlyAspSerCysPro......HisGlySe 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....SerProLeuPheIlePheMetArgArgSerSerLeuLeuSerAr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 ArgGluGlyArgGlnLeuGlnPro.....AlaGluArgPr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rProGlnGlyProLeu...AlaProProAlaSerProGlyProPheAlaT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AAA58472 from: 1 to: 18660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 27.604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                             Claim 8; Page 137-153; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-508-832-10 x AAA58472/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 1.333
Percent Similarity: 43.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 112.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 hrArg.....
    2000-465974/40.
B; AAB07580, AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
      WPI; 20(
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
    Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.
                                                                                                                                                                                                                                                                                                                                      BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA58472
1749 ACCGTCCATGAAACCCAAACCTGCCTCAGTGGATGCCAACACCAAGCTGA 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_except= (pos: 1..3, aa: Met)
note= "ORF31; encodes AAB07580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Lransl_except= (pos: 1..3, aa: Met)
/note= "ORF37; encodes AAB07586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rransl_except* (pos: 1..3, aa: Wet)
/note* "ORR39; encodes AAB07588*
17646..18659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "ORF40; encodes AAB07589"
/note- "no termination codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note- "ORF34; encodes AAB07583"
11888..12640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= h
/note= "ORF38; encodes AAB07587"
16476..17462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "ORF32; encodes AAB07581"
9447..10802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag- c
//note= "ORF33; encodes AAB07582"
/*tag- d
/*tag- d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards
                                                              1699 CGCGGTCACTGCCTGCCAGGTCTACGTGAATCAT 1665
                                        116 hrProSerProProCysGlnAlaPhe...AsnHis 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanchez C, Chen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                         seq_documentation_block:
ID AAA58472 standard; DNA; 18660 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "un.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JAN-1999; 99US-0115435.
05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-2000; 2000WO-US00445.
                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              925..9450
                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces verticillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Du L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200040704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-2000
                                                                                                                                                                                                                     AAA58472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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92

us-09-508-832-10.rng

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fusion protein.
    S \lesssim S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein; fusion protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots .
                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseg/geneseqn-embl/NA2001A.DAT:AA166848
..CGACGTCGAGGGACAG 6298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bjorn SP, Thastrup O, Almholt DC;
                                                                                                       141 pMetArgProGluIleTrpIleAlaGlnGluLeuArgArgIleGlyAspC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of HSPDE4A4catD-EGFP fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 142-147; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..3090
/note- "fusion protein"
                                                                                                                                                                                                                                                                                                                             6297 GTCGAACCGGCTGGTCACACCGCCGA 6272
                                                                                                                                                                                                                                                       158 luPheAsnAlaTyrTyrAlaArgArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAI66848 standard; DNA; 3090 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2001; 2001WO-DK00264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-0000849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terry BR, Scudder KM,
Praestegaard M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-611727/70.
P-PSDB; AAG65779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200179526-A2.
                                                                                                                                                                                 6320 CCCGAGA.
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492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 aProMetSerCysAspLysSerThrGlnThrProSerProProCysGlnA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 laPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 CTCATCGTAACACCATTTGCTCAGGTGCTGGCCAGCCTCCGGAGCGTCCG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441
                                                                                                                                                                                                                                                                                                                                                 195 AGGCGCCGATGCCATGGACACCAGCGACCGGCCCGGCTGCGCACGA 244
                                                                                                                                                                                                                                                                                                                                                                                                    35 erLeuGlnThrGluProGln......GlyAsnProGluGly 46
                                                                                                                                                                                                                                                                                                                                                                                                                                             245 CCCGCATGTCCTGGCCCTCGTCCTTCCATGGCACTGGCACCGGCAGCGGC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 GGCGCGGCGCGCGCAGCAGCGCGCTTCGAGGCAGAGATGGGCCGAC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                             6 SerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGlnProAl 22
                                                                                                                                                                                                                                                                                      47 ASRHISGlyGly......GluGlyAspSerCysProH1 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 aGluArgProProGlnLeu......ArgProGlyAlaProThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 heAlaThrArgSerProLeuPheIlePheMetArgArgSerSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 GACCATGTCCCGGAAC.....
Sequence 3090 BP; 791 A; 900 C; 807 G; 592 T; 0 other;
                                                                          Length: 171
Gaps: 7
Percent Identity: 27.485
                                                                                                                                                                                                           Align seg 1/1 to: AAI66848 from: 1 to: 3090
                                                                        111.50
1.282
50.877
                                                                                                                                                  alignment_block:
US-09-508-832-10 x AAI66848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 yAspGluPheAsn 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 TAGCAACTTCTCA 588
                                                                            Quality:
                                                                                                              Percent Similarity:
                                                                                             Katio
                                                         alignment_scores:
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12.65
12.65
12.65
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12.65
                                                                                                                                                                                                                                            seq_documentation_block:
Sequence 64, Application Us/08474379C
Sequence 65, Application Us/08474379C
Sexeral Information:
APPLICANT: Wigler, Michael H.
APPLICANT: Wigler, Michael H.
TITLE OF INVENTION: CLONING BY COMPLENENTATION AND RELATED TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 SerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGlnProAl 22
       /cgn2_6/ptcdata/1/ina/5B_COMB.seq:US-08-231-193A-43 + 101.50
/cgn2_6/ptcdata/1/ina/5B_COMB.seq:US-08-486-273A-43 + 101.50
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:US-08-480-474-43 + 101.50
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:US-08-940-086A-43 + 101.50
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:US-08-940-086A-43 + 101.50
                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-474-379C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPTRIES TO THIE STATES OF AMELICA COUNTRIES OF COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk COMPUTER: ENDORTHIALS COMPUTER: ENDORTHIALS COMPUTER: ENDORTHIALS PACENCY OF COMPUTER: ENDORTHIALS PACENCY OF ELSOS SOFTWARE: ENDORTHIALS APPLICATION NUMBER: US/06/474,379C
FILING DATE: 07-JUN-1995
CLASSIPICATION NUMBER: US/06/188
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION NUMBER: US 08/206,188
FILING DATE: 19-APR-1991
APPLICATION NUMBER: US 08/206,188
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAT'A:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 38,107
REFERENCE/DOCKET NUMBER: 27866/32771
PELECHONE: (310,100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 3705
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Percent Identity: 27.485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Marshall, O'Toole, Gerstein, Murray 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 25 CITY: Chicago STATE: Illinois COUNTRY: United States of America TIP: 6606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-474-379C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-508-832-10 x US-08-474-379C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 64
SEQUENCE CHARACTERRETICS:
LENGTH: 3705 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 111.50
Ratio: 1.282
nilarity: 50.877
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-474-379C-64
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**COPPLIATE**

**COPPLIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                            Command line parameters:
-QOCOMMAND LINE PAIN MODEL-Frame+_D2n model-DEV-X1h
-QO-/CGD2_L1/USFTO_SPOOL/USG9508832/runat_06082002_103611_2799/app_query.fasta_1.259
-D8-ISSUGG_R2TO_SPOOL/USG9508832/runat_06082002_103611_2799/app_query.fasta_1.259
-D8-ISSUGG_RAERTE_NA -QFWT-Fastap -SUFFIX=rn1 -GAPOP=12.000
-GAPOP=4.500 -NINAWTH=0.100 -LOOPCE_0.000 -LOOPCE_0.000
-GAPOP=4.500 -GCAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=4.500 -GCAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FCAPEXT=7.000 -STAFT=1 -MATRIX=blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-NON-PFC
-THR_MAX=100 -THR_MIN=0 -ALIGN-15 -MODE=LOCAL -OUTFNT=PFC
-THR_MAX=100 -THR_MIN=0 -MAIGN-15 -MODE=LOCAL -OUTFNT=PFC
-USBR=-US99508832_ECGN1_1 46 -NCPU-6 -ICPU-3 -LONGLOG
-USBR=-US99508812_ECGN1_1 46 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT=120 -WARR_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
       out_format : pfs
                                                                                                                                software, version 4.5,
OM of: US-09-508-832-10 to: Issued_Patents_NA:*
                                                                                                                         About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Query: US-09-508-813-10
Query length: 198
Database: ISsued_Patents_NA:*
Database sequences: 381533
Database length: 122816752
Search time (sec): 46.200000
                                                            Date: Aug 7, 2002 10:36 PM
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360 CCCGCATGTCCTTCCTTCCATGCCACTGGCACCGCCACGCGCC 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 receacacecegacececaacececaacececacececacecear 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 AsnHisGlyGly......GluGlyAspSerCysProH1 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 sGlySerPro...GlnGlyProLeuAlaProProAlaSerProGlyProP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 healaThrArgSerProLeuPheIlePheMetArgArgSerSerLeuLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-146-249A-64 from: 1 to: 3705
                                                                                                                                                                                                                                                                                                                              Gaps: 7
Percent Identity: 27.485
                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-508-832-10 x US-09-146-249A-64
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          Quality: 111.50
Ratio: 1.282
Percent Similarity: 50.877
                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 116..2774
US-09-146-249A-64
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                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                alignment_scores:
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us-09-508-832-10.rni

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seq_documentation_block:
Sequence 64, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Migler Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF EXPERIENCE CLONING BY COMPLESSPONDENCE ADDRESS:
ADDRESSPEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 SerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGlnProAl 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 erLeuGlnThrGluProGln.........GlyAsnProGluGly 46
                                                                                                                                                                                                               AUDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6100 Sears Tower, 233 South Wacker Drive STATE: Illinois
seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-206-188B-64
                                                                                                                                                                                                                                                                                                                       STATE: United States of America COUNTRY: United States of America 2.10: 60606-6402

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EMP FC compatible COMPUTER: IBM FC compatible SOFTWARE: PatentIn Release #1.0, version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/206,188B FILING DATE: 01-WAR-1994
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-206-188B-64 from: 1 to: 3705
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Percent Identity: 27.485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-ARR-1990
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-508-832-10 x US-08-206-188B-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ 1D NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 3705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 111.50
Ratio: 1.282
Percent Similarity: 50.877
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: LOCATION: 116..2774
US-08-206-188B-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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seq_documentation_block:
 Sequence l15, Application US/08997080
 Sequence l15, Application US/08997080
 Patent No. 596854
 GENERAL INFORMATION:
 APPLICANT: WATSON JAMES D.
 APPLICANT: WATSON JAMES D.
 APPLICANT: WATSON WETHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY NUMBER OF SEQUENCES: 194
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Ann W. Speckman
 STREET: 2601 Elliott Avenue, Suite 4185
 CITT: Seattle 123 laPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139 90 SerArgSerSerSerGlyTyrPheSerPheAspThrAspArgSerProAl 106 106 aProMetSerCysAspLysSerThrGlnThrProSerProProCysGlnA 123 607 410 GGCGCGGGCGGAGGCAGCAGGCGCTTCGAGGCAGAGAATGGGCCGAC 459 47 AsnHisGlyGly......GluGlyAspSerCysProHl 57 seq_name: /cgn2_6/ptodata/1/lna/5B_COMB.seq:US-08-997-080-115 57 sGlySerPro...GlnGlyProLeuAlaProProAlaSerProGlyProP SOFTWARE: FastSEC for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080 ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Jane
RESISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565 115: COMPUTER READABLE FORM:
NEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 647 base pairs TYPE: nucleic acid TELEFAX: 206-269-0563 CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 691 TAGCAACTTCTCA 703 156 yaspGluPheAsn 160 USA FILING DATE: ZIP: 98121 COUNTRY:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION WOMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILLING DATE: U.S. Patent Application No. 5985287 08/705,347 ATTORNEY/ACRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111 (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (1111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111) (111)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 oProAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheM 83
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Gaps: 9
Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-997-362-115 from: 1 to: 647
                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
STEMBRE: FRSESSO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
        STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sleath, Janet
REGISTATION UNDHER: 37,007
REFERENCE/COCKET UNDHER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFRY: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-508-832-10 x US-08-997-362-115
                                                                                                                                                  ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 647 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107.00
1.259
52.469
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                                                Seattle
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Ratio:
Percent Similarity:
                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : MOLECULE TYPE:
US-08-997-362-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
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APPLICANT: Hiyama, Jun
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margor
APPLICANT: Scott, Linda
APPLICANT: Scott, Linda
APPLICANT: Cort, COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
COMPRESORDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 ...TCAAAGAGGTCGCCAAGAAGACCGACGACGTCGCGGGGGGGCGCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 rProSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlas 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: ::: III :::IIIII IIIIII::: III 315 CGCCCACCCGCCCCAACCCGCT.....CGCCCTCAAGCGTGGCATCG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 AspThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnTh 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 ACCACCCCACCGTCCTCGCTCACCTTCGCGAAGGCCTGCGCAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 erMetArgGlnAla.GluProAlaAspMetArgProGluIleTrp..... 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 ......1leAlaGlnGluLeuArgArgIleG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AACGCCCTCGCAGACG......CCGTAAAGGTGACGTTGGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaPr 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 etArgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPhe 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ArgGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaPr 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AGACAATTGCGTATGACGAAGAGGCCCGCCGTGGCCTCGAGCGGGGCCTC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/ina/58_COMB.seq:US-08-997-362-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 oThrSerLeuGlnThrGluProGlnGlyAsnPro.GluGlyAsnHisGly
                                                                                                                                                                                                                                                                                                                     Gaps: 9
Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 647
                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 GTCGAGACCAAGGAGCAGATTTCTGCCACCGC 440
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Sequence 115, Application US/08997362;
Patient No. 5885287;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-997-080-115
                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-508-832-10 x US-08-997-080-115
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: Genomic RNA
US-08-997-080-115
                                                                                                                                                                                                                                                                     107.00
1.259
52.469
                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                      alignment_scores
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alignment_block:
US-09-508-832-10 x US-09-095-855-115
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US-09-324-542-115
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Quality:
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                                                                                     133 erMetArgGlnAla.GluProAlaAspMetArgProGluIleTrp..... 147
                                                                                                                                   315 CGTCGCAGCCGCCAACCGCT.....CGGCCTCAAGCGTGGCATCG 358
                                                                                                                                                                                                                                                            148 ......1lealaGlnGluLeuArgArgileG 156
                                                                                                                                                                                                                                                                                                                   359 AGAAGGCTGTCGAGGCTGTCACCCGAGCGTGTCGCCAAGGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-095-855-115
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Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: The Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Law Offices of Ann W. Speckman
STRET: 2601 Elliott Avenue, Sulte 4185
STATE: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            156 lyAspGluPheAsnAlaTyrTyrAlaArgArg 166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER, 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 12-DE-1997
ATTORNEY/AGBNT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/OGCKET NUMBER: 37,007
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : MOLECULE TYPE: Genomic RNA
US-09-095-855-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 647 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 107.00
Ratio: 1.259
milarity: 52.469
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TOPOLOGY: 11r
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seq_documentation_block:

Sequence 115, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestides, Ross

TTLE OF INVENTION: Wethods and Compounds for the Treatment

TITLE OF INVENTION: Wethods and Compounds for the Treatment

TITLE OF INVENTION: Wethods and Compounds for the Treatment

TITLE OF INVENTION: Wethods and Compounds for the Treatment

TITLE OF INVENTION: Wethods and Compounds for the Treatment

TITLE OF INVENTION: Wethods and Compounds for the Treatment

TITLE OF INVENTION OF Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

BARLIER FILING DATE: 1997-112-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PastSEQ for Windows Version 3.0

IRMAGINATE: AND 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 CCCGAAGGTCGCAACGTCGTGCTGGAGAAGAGTGGGGCG......CC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 ACCACCGCACCGTCGCTCAGGCTCTGGTGGCGAGGCCTGCGCAA 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 ...TCAAAGAGGTCGCCAAGAAGACCGACGACGTCGCGGGGGGCGACGCCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 rProSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                 33 oThrSerLeuGlnThrGluProGlnGlyAsnPro.GluGlyAsnHisGly 49 | 11 | 11111 | 1111158 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaPr 66
                                                                                                                                           17 ArgGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaPr 33
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                                                                                                                                                                                                                                                                                      8 AGACAATTGCGTATGACGAAGAGGCCCGCGGGGCCTCGAGCGGGGCCTC
Align seg 1/1 to: US-09-095-855-115 from: 1 to: 647
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Percent Identity: 30.864

Percent Similarity: 52.469

516 CGTCGAGCCCC......CGC 503 402 ATACCCGTGCATCAAAACGAACACCGGGTTGCCCCCAGCGCGCGGGGCCCA 353 92 SerSerSerGlyTyrPheSer....PheAspThrAs 102 502 TCTCCCCGTGGCCCCGGAAGTCGAACACAACCACCGGGTACCCCCACTCC 453 102 parqSerProAlaProMetSerCysAspLysSerThrGln.ThrProSer 118 119 ProProCysClnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetAr 135 707 ATGACGTCCCGGAGCCTATAGTACGGGCTATCAGCAGCCACCGCGT...A 661 610 TGAACCCCACCAATATTATCCGGCGGGCCGGGGAACCGCTCCGAGACATAG 561 660 GACCCGCGGGTCCCCAGCACCCTCCACGATCGCTACAGCGCCGCCCATAC 611 14 ArgGluGlyArgGlnLeuGlnProAlaGluArgProProGlnLeuA 29 29 rgProGlyAla......ProThrSerLeuGlnThrGluProGln 41 42 GlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGl 58 58 ySerProGlnGlyProLeuAlaProProAlaSerProGlyProPheAlaT 75 75 hrargSerProLeuPheIlePheMetArgArgSerSerLeuLeuSerArg 91 from: 1 Gaps: 9 Percent Identity: 27.684 Align seg 1/1 to reverse of: US-08-602-359A-24 09010/010001 OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/602,359A FILING DATE: February 16, 1996 alignment_block: US-09-508-832-10 x US-08-602-359A-24/rev REFERENCE/DOCKET NUMBER: 0901
TELECOMONICICATION INFORMATION:
TELEPRONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1041 NUCLECTIDES
TYPE: NUCLEIC ACLD
STRANDEDNESS: SINGLE FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HALLE, LISA A.
RECISTRATION NUMBER: 38,347 TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE TOPOLOCY: LINEAR MOLECULE TYPE: GENOMIC DNA 1.244 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: Quality: 107.00 Ratio: 1.244 Percent Similarity: 48.588 US-08-602-359A-24 alignment_scores

135 gGlnAlaGluPro.....AlaAspMetArg.....ProGluIleT 147

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seq_documentation_block:
Sequence 113, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Faul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TARTHEMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2501 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
  11
..cc 135
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                                                                                                                                                                                                                                                                                                                                                        116 rProSerProProCysGlnAlaPhcAsnHisTyrLeuScrAlaMetAlaS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 AGAAGGCTGTCGAGGCTGTCACCCAGTCGCTGAAGTCGGCCAAGGAG 408
                                                                                                                                                                                          118 ...TCAAAGAGGTCGCCAAGAAGACCGACGACGGCGGGGGGGCGCCC 264
                                                                                                                                                                                                                                                                                                                                                                                           265 ACCACCGCCACCGTCGCTCAGGCTCTGGTTCGCGAAGGCCTGCGCAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......IleAlaGlnGluLeuArgArgIleG 156
                                                                66 oProAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheM 83
                                                                                                                                                                83 etArgArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPhe 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/lna/5B_COMB.seq:US-08-997-362-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 ermetargGlnAla.GluProAlaAspMetArgProGluIleTrp.....
  93 CCCGAAGGGTCGCAACGTCGTGGAGAAGAAGAAGGGCGCC...
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                                                                                                             136 CCCACGATCACCA...ACGATGGTGTGTCCATCGCCA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REPERNIC/DOCKET NUMBER: 11000.1002c2
TELECONMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 lyAspGluPheAsnAlaTyrTyrAlaArgArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 GTCGAGACCAAGGAGCAGTTTCTGCCACCGC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z1P: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Disket1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: W. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                  Sequence 113, Application US/08997080

Sequence 113, Application US/08997080

Patent No. 596654

GENERAL INFORMATION:

APPLICANT: WATSON, JAMES D.

APPLICANT: TAN, PAUL L.J.

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-

CORRESPONDENCE: 194

CORRESPONDENCE: LAW Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CTRY: Seattle

STATE: WA

COUNTRY: USA
352 GCACCCCAGCCCCGAACCACCACCCACCCCGCGGTCACCTCT 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaPr 66
                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-997-080-113
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Gaps: 9
Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11000.1007
                                                                147 rplieAlaGlnGluLeuArgArglleGly 156
                                                                                             302 TTGTAGGTGAGCCCCTCCGGCGCAACGGG 274
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APPLICATION NUMBER: US/08/997,080
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-997-080-113
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US-09-508-832-10 x US-08-997-080-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATORNEY/AGENT IRFORMATION:
NAME: Sleath, Janek
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0563
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ 1D NO: 113: SEQUENCE CHRACTERISTICS: LENGTH: 1569 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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; MOLECULE TYPE: Genomic DNA
US-08-997-080-113
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Ratio: 1.259
nilarity: 52.469
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                             seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98121
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us-09-508-832-10.rni

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93 CCCGAAGGCTCGCAACGTCGTGCTGCAGAAGTCGCCCC.....CC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 ...TCAAAGGGCCCCAAGAAGACCGACGACGTCGCGGGGGGCGCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 rProSerProProCysGlnAlaPheAsnHLsTyrLeuSerAlaMetAlaS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 ACCACCGCCACCGTGCTCAGGCTCTGCTTCGCGAAGGCCTGCGCAA 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 AACCCCTCGCAGACG.......CCGTAAAGGTGACGTTGGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oProAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheM 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 ArgGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaPr 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/1na/6B_COMB.seq:US-09-095-855-113
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Percent Identity: 30,864
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Patent No. 6166093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Viser, Elizabeth
APPLICANT: Sinner, Margot,
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-997-362-113
                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-508-832-10 x US-08-997-362-113
                                       INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: Genomic DNA
US-08-997-362-113
                                                                                                                                                                                                                                                                                                     107.00
1.259
52.469
TELEFAX: 206-269-0563
TELEX:
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                                                                                                                                                                                                                                                                                  alignment_scores:
   Quality:
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Percent Similarity:
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TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 oThrSerLeuGlnThrGluProGlnGlyAsnPro.GluGlyAsnHisGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 AACGCCTCGCAGACG...........CCGTAAAGGTGACGTTGGG 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ArgClnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaPr 33
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Gaps: 9
Percent Identity: 30.864
                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER: 1219: 1218/2121
COMPUTER: 1218/212121212
COMPUTER: 1218/21212
COMPUTER: 1218/21212
COMPUTER: 1218/21212
COMPUTER: 1218/22
COMPUTER: 1218/22
COMPUTER: 1218/22
COMPUTER: 1218/22
APPLICATION NUMBER: US/09/095,855
                                                             ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11000.1002c3
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-ANG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILTAN DATE: 12-108-1397, 362

PELING DATE: 23-DEC-1997

ATTORNEY/AGENT INCRAMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007

TELECOMMUNICATION INCOMATION:
TELECOMMUNICATION INCOMATION:
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US-09-508-832-10 x US-09-095-855-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: Genomic DNA US-09-095-855-113
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1.259
52.469
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                                                               ADDALL
STREET: 200.
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    Quality: 1
    Ratio: 1
Percent Similarity: 5
                                                                                                                                                USA
                                                                                                                        STATE: W.
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us-09-508-832-10.rni

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seq_documentation_block:
Sequence 113. Application US/09324542
Sequence 113. Application US/09324542
Sequence 113. Application US/09324542
Sequence 110. Seq
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                                                                                                                                                                                                                                                                                                                   116 rProSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaS 133
                                                                                                                                                                                                                                                                                                                                                                                                                          265 ACCACCACCACCACCACCTCAGGCTCTGGTTCGCGAAGGCCTGGGCAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ......IlealaGlnGluLeuArgArgIleG 156
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                                                                                                                                                                  218 ...TCAAAGAGGTCGCCAAGAAGACCGACGACGTCGCGGGGGGGCGCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 othrSerLeuGlnThrGluProGlnGlyAsnPro.GluGlyAsnHisGly 49 | 11 | 11111 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 |
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                   66 oProAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheM 83
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Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 GTCGAGACCAAGGAGCAGATTCTGCCACCGC 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-508-832-10 x US-09-324-542-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mycobacterium vaccae
US-09-324-542-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 107.00
Ratio: 1.259
Percent Similarity: 52.469
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APPLICANT: WAISON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLYCORRESPONDENCE ADDRESS: 194
CORRESPONDENCE ADDRESS: 218 ...TCAAAGAGGTCGCCAAGAAGACCGACGACGACGACGGCGGGGGGCGACC 264 133 erMetArgGlnAla.GluProAlaAspMetArgProGluIleTrp..... 147 148IlealaGlnGluLeuArgArgIleG 156 359 AGAAGGCTGTCGAGGCTGTCACCCGGTGCTGCAAGTCGCCAAGGAG 408 170 ..AGGAGATCGAGCTGGAGGACCCGTACGAGAAGATCGGCGCTGAGCTGG 217 seq_name: /cgn2_6/ptodata/l/ina/5B_COMB.seq:US-08-997-080-159 100 AspThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnTh Percent Identity: 30.864 ZIF: 99121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAILINE
OPERATING SYSTEM: DOS
SUSTWARE: FastSEG for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080 ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 STATE: Seattle STATE: USA 156 lyAspGluPheAsnAlaTyrTyrAlaArgArg 166 409 GTCGAGACCAAGGAGCAGATTTCTGCCACCGC 440 11000.1007 FILING DATE:
CLASTELATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 31each
REGISTRATION NUMBER: 37.007
REFERENCE/OCKET NUMBER: 11000
RELECHONE: 206-269-0565
TELEPHONE: 206-269-0565 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 1626 Base pairs TYPE: nucleic acid strandedness; single Quality: 107.00 Ratio: 1.259 nilarity: 52.469 Ratio: Percent Similarity: alignment_scores:

us-09-508-832-10.rni

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
ATORNEY/ACENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 17,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION LINCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 CCCGAAGGGTCGCAAGGTCGTGCTGCAAAGAAGTGGCCCC......CC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 ..AGGAGATCGAGCTGGAGGACCCGTACGAGAAGATCGGCGCTGAGCTGG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......llealaGlnGluLeuArgArglleG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 AGAAGGCTGTCGAGGCTGTCACCCAGTCGCTGAAGTCGGCCAAGGAG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 rProSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SB AACGCCTCGCAGAGG..........CCGTAAAGGTGGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 oproAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheM 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ArgClnLeuGlnProAlaGluArgProProClnLeuArgProClyAlaPr 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 oThrSerLeuGlnThrGluProGlnGlyAsnPro.GluGlyAsnHisGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaPr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AGACAATTGCGTATGACGAAGAGGCCCGCGCGTGGCCTCGAGCGGGGCCTC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-997-362-159 from: 1 to: 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 162
Gaps: 9
Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 lyaspGluPheAsnalaTyrTyrAlaArgArg 166
        APPLICATION NUMBER: US/08/997,362 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-508-832-10 x US-08-997-362-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 107.00
Ratio: 1.259
Percent Similarity: 52.469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 CCCGAAGGGTCGCAACGTCGTGCTGGAGAAGAAGTGGGGCG......CC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
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                                                                                                                                                                                                                                                                                                                                      33 oThrSerLeuGlnThrGluProGlnGlyAsnPro.GluGlyAsnHisGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                     58 AACGCCCTCGCAGACG......CCGTAAAGGTGACGTTGGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaPr 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 etArgArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPhe 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 GrcGAGACCAAGGAGCAGATTTCTGCCACCGC 440
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US-09-508-832-10 x US-08-997-080-159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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359 AGAAGGCTGTCGAGGCTGTCACCCAGTCGCTGCTGAAGTCGGCCAAGGAG 408
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                                            93 CCCGAAGGGTCGCAACGTCGTGCTGGAGAAGAGTGGGGCG......CC 135
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                                                                                                                                                                                                                                                                                                             66 oproAlaSerProGlyProPhealaThrargSerProLeuPheIlePhem 83
                                                                                                                                                                                     83 etArgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPhe 99
50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaPr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 lyAspGluPheAsnAlaTyrTyrAlaArgArg 166
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    Sequence 159, Application US/09095855
    Patent No. 6160093
    Patent No. 6160093
    GENERAL INFORMATION:
    APPLICANT: Tan, Paul
    APPLICANT: Stinner, Margot
    APPLICANT: Stinner, Margot
    APPLICANT: Stoner, Margot
    APPLICANT: Score Compounds and Methods for
    TITLE OF INVENTION: Compounds and Methods for
    TITLE OF INVENTION: Treatment and Diagnosis of Nycobacterial Infections
    NUMBER OF SEQUENCES: 208
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Law Offices of Ann W. Speckman
    STREET: 2601 Elliott Avenue, Suite 4185
    CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ArgGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaPr 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-095-855-159 from: 1 to: 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 9
Percent Identity: 30.864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENUTER: IBM Compatible
OMENATING SYSTEM: DOS
SOFTWARE: FRALED for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-40G-1996
APPLICATION NUMBER: 08/73,970
FILING DATE: 12-70N-1997
APPLICATION NUMBER: 08/873,970
FILING DATE: 29-60-1997
APPLICATION NUMBER: 37-007
RECISTRATION NUMBER: 31-007
RELECHOME: 206-269-0563
FILING DATE: 206-269-0563
409 GTCGAGACCAAGGAGCAGATTTCTGCCACCGC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-508-832-10 x US-09-095-855-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRA.

2.1P: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
Compatible
TOWN TYPE: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHRACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality: 107.00
Quality: 1.259
Percent Similarity: 52.469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-09-095-855-159
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| BI463212 603207993F1 NIH_MG
| AL244043 Terraodon nigroviri
| BF627834 HVSMED0005020f Hord
| BF637834 BO2142365F1 NIH_MG
| BG843632 1024003E09.x2 C. r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and the FAREN Genome Exploration Research Group Phase II Team and the FARTOM Consortium.

Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001).

In Genome 10, 1006).

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(carinci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)
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MUS musculus 10 days embryo whole body cDNA, RIKEN full-length
MUS musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610020M23:BCL2-like 11 (apoptosis
faciltator), full insert sequence.
AKO11490.
AKO1490.1 GI:12847647
HTC: CAP trapper.
HTC: CAP trapper.
Clone.lib:RIKEN full-length enriched mouse CDNA to mRNA,
clone:2610020M23.
Clone:2610020M23.
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MAMMADIAL ENTELEOSTOM SCIUROGNATH; MUTIdae; Mus.
MAMMADIAL SULHeria; Rodentia; Sciurognath; Muridae; Mus.
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cjoning
Meth. Enzymol. 303, 19-44 (1999)
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-NOPH-6 -ICPU-3 -LONGXLOG -DEV_TIMEOUT=120 -MARN_TIMEOUT=30
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                                                                                                                       Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGACGATCCAAGAGCTTTTTTTTTTTTYN 3], CDNA was prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5].
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1. .1206
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              .1206
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US-09-508-832-10 x AK011490
                                                                                                                                                                                                                                                                                                                                                                                                  Host: SOLR.
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
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                                                                                      COMMENT
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BG921698 935 bp mRNA linear EST 05-JUN-2001 602825518F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4954300 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

283 c 276 g 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex--female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_nost-*pHi08*
134 MetargGlnAla.....GluProAlaAspMetArgProGluIleTrpII 148
                                                                                                             605 ATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCGGAGATACGGAT 654
                                                                                                                                                                                                 165 rgArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMet 181
                                                                                                                                                                                                             /organism-*Mus musculus*
/strain-*ryB/N*
/db_xref-texon:10090*
/clone="IMAGE:4954300*
/clone_llb="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BC921698
BG921698.1 GI:14302174
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/Lissue_Lype="corebellum"
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/lab_host="0 day 
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 645)
Arakawa.T., Carninci.P., Fukuda.S., Furuno.M., Hanagaki.T., Hara.A.
HIramoto,K., Hori,F., Ishij,Y., Ito,M., Kawai.J., Ronno,H., Rouda
,M., Koya.S., Matsuyama.T., Miyazaki,A., Nomura.K., Ohno,M.,
Okazaki.Y., Okido,T., Saito,R., Sakai.K., Sanai.K., Sanai.H., Saski.
D., Shibata.K., Shinagawa.A., Takahashi.F., Takeda.Y., Fanaka.T., Toya,T.,
Muzamatsu.M. and Hayashizaki.Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Contect: Yoshihide Hayashizaki
Luboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suchino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--184-format sequencing pipeline with 184 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. and Hayashizaki, Y. computer-based methods for the mouse full length cDNA encyclopedia: real time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
Wagii,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watafiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.rlken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualiflers
1. .645
1. .645
Action="Mus musculus"
Ab_xref="taxon:10090"
Ab_xref="taxon:10090"
Ab_xref="taxon:10090"
Action=_10="taxon:10090"
Action=_10="taxon:1009
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                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
COMMENT
                                                         REFERENCE
AUTHORS
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LOCUS BB651225
DEFINITION BB651225 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus CDNA clone C230069E03 5', mRNA sequence.
ACCESSION BB651225
VERSION BB651225, GI:16485479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 spThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ArgArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArgMe 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       695 AGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACACCCTCAAATG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluGlyAspSerCysProHisGly.SerProGlnGlyProLeuAlaProP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetalaLysGlnProSerAspValSerSerGluCysAspArgGluGlyAr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 roAlaSerProGlyPro.PheAlaThrArgSerProLeuPhellePheMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 tVal.IleLeuArgLeuLeuArgTyrIleValArgLeuValTrp 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 GITATCTTACAAACGTGTTACCCTTTATCTTCCGTCTGGTATGG 788
                                                                                                                                                                                        Length: 200
Gaps: 5
Percent Identlty: 81.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 935
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                                                                                                                                                                                                                                       4.435
                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-508-832-10 x BG921698
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Percent Similarity:
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VERSION
KEYWORDS
SOURCE
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Email: szhooetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pdejongémail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.thgr.org/tdb/bac_ends/mouse/bac_end_intro.html)
Plate: 227 row: P column: 3
Seq primer: 17
Closs BAC ends.
   rel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Source
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AZ706148.1 GI:12433319 GSS 24-JAN-2001 GBCI-23-227P3, GSS 24-JAN-2001 GBCI-23-227P3, GSS 24-JAN-2001 GSS 24-JAN-200
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Mouse BAC End Sequences from Library RPCI-23
Mopublished (1989)
Other_GSSs: RPCI-23-227P3.TJ
Contact: Shaying Zhao
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota: Netazoa: Chordata: Cranlata: Vertebrata: Euteleostomi:
Mammalla: Eutherla: Rodentia: Sciurognathi: Muridae; Musimus: Musimus in Chases I to 580)

| (bases I to 580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 ACAATTGCAGCCTGCTGAGAGGCCTCCCCAGCTCAGGCCTGGGGCCCCTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 hrSerLeuGlaThrGluProGlnGlyAsaProGluGlyAsaHisGlyGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 -gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT 34
                                                                                                                                                                                                     Percent Identity: 89,726
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                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                       to: 645
                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                  667.00
4.869
93.836
                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BB651225
                                                                                                                                                                                                                                                                                alignment_block:
US-09-508-832-10 x BB651225
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LOCUS AZ706148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                          Quality:
                                                                                                                                                                                                     Percent Similarity:
                                                                                                      alignment_scores
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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ORIGIN
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/note-note and Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially disested
with a combination of EcoRI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrPr 117
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Percent Identity: 93.893
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Location/Qualifiers
1.580
/organism="Hus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/scx="Female"
/lab_host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="host="hos
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5.248
95.420
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US-09-508-832-10 x AZ706148
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seq_documentation_block:
LOCUS B1906766 700 bp mRNA linear EST 16-OCT-2001
DEFINITION 603064506F1 NIH_MCC_118 Homo sapiens cDNA clone IMAGE:5213713 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 rgArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ThraspargSerProAlaProMetSerCysAspLysSerThrGlnThrPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                              507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePheMetA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 131
Gaps: 1
Percent Identity: 93.130
                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: BB577135 from: 1 to: 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B1906766.1 GI:16169524
                                                                                                                                                                                                                                                                                                                      653.00
5.224
95.420
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US-09-508-832-10 x BB577135
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B1906766
                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                           alignment_scores:
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VERSION
KEYWORDS
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ORIGIN
                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Knddo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, T., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                             BB577135 RIKEN full-length enriched, 13 days embryo male testis Mus musculus cDNA clone 6030401M20 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Bincyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Namm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/cione="6030401M20"
/cione_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="testis"
/dev_stage="13 days embryo"
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                                                                                           BB577135.2 GI:16449433
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seq_name: gb_est1:BB577135
                        seq_documentation_block:
LOCUS BB577135
                                                                                                                                   Mus musculus
                                        LOCUS
                                                                           ACCESSION
VERSION
KEYWORDS
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AUTHORS
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9

Thu Aug

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seq_name: gb_est2:BF021B82
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Laukocyte"
/lab_host='DHIOB"
/note='Vector: pCNV-SPORT6; Site_1: NotI; Site_2: ECORV
/note='Vector: pCNV-SPORT6; Site_1: NotI; Site_2: ECORV
(destroyed): RNA Source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (ECORV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
                               Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi; Gases I to 700)

1 (bases I to 700)

2 I (bases I to 700)

3 NIH MGC http://mgc.ncl.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

4 Unpublished (1999)

5 Unpublished (1999)

5 Unpublished (1999)

6 Unpublished Experiments of Health, Mammalian Gene Collection (MGC)

7 Issue Procurement: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.
CLone distribution inc Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Righ quality sequence stop: 696.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Consortium/LNL at:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 ATGGCAAAGCAACCTTCTGATGTAAGTTCCTGAGTGTGACCGAGAAGGTA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetalaLysGlnProSerAspValSerSer.GluCysAspArgGluGlyA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 rgGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 151
Gaps: 2
Percent Identity: 95.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: B1906766 from: 1 to: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_118"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            651.50
4.402
98.013
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US-09-508-832-10 x BI906766
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Ratio:
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                      ORGANISM
                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
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ORIGIN
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SOURCE
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117 TOSEPTOALEY CORSESTIONARY DESCRIPTION THIS INTELLIGITIES INTELLIGITI
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seq_documentation_block:
LOCUS B1454637
DEFINITION 603170532F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5280271 5',
Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Musculus
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Bukaryota: Metazoa: Chordata: Sciurognathi: Muridae: Murinae: Nus.
1 (Dases 1 to 76)
NIH-MSC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                   uSerAlaMetAlaSerWetArgGlnAla....GluProAlaAspMetA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 AsnalaTyrTyrAlaArgArgValPheLeuAsnAsnTyrGlnAlaAlaGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                    78 oLeuPhellePheNetArgArgSerSerLeuLeuSerArgSerSerG
                                                                                                                        Length: 139 Gaps: 1 Percent Identity: 85.612
                                                                                                                                                                                                                           to: 452
                                                                                                                                                                                                                           Align seg 1/1 to: BF021882 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
B1454637
B1454637.1 GI:15245293
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4.822
92.806
                                                                                                                                                                            alignment_block:
US-09-508-832-10 x BF021882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est2:BI454637
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                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                     106
                                                                                                             alignment_scores
                                                    BASE COUNT
ORIGIN
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
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/clone="IMAGE:525071"
/clone="IMAGE:525071"
/clone="Lype="tumor, gross tissue"
/dev_stage="tumor, gross tissue"
/dev_stage="tu
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics. Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LiAMIGI row: o column: 08
High quality sequence stop: 760.
Location/Qualifiers
I. 765 Mus musculus*
//strain-c57/86*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294
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Percent Identity: 59.701
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4.465
64.179
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US-09-508-832-10 x B1454637
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Ratio:
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23 ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAAGGTGG 272
1 MetalaLysClnProSeraspValSerSerGluCysaspargGluGlyar 17
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JOURNAL
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BG173095 668 bp mRNA linear EST 06-FEB-2001
DEFINITION 602336666F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4459720 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-*Organ: mammary: Vector: pCMV-SPORT6; Site_1: Salf; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library: constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH* 215 c 162 g 136 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Nus.
1 (bases 1 to 668)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: capabs.remail.nih.gov
Contact: Robert Strausberg, Ph.D.
Email: capabs.remail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://mage.llni.gov
Plate: LLAM10260 row: c column: 17
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone=lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="lo months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544.50 Length: 154
4.125 Gaps: 8
85.714 Percent Identity: 77.273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-508-832-10 x BG173095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BG173095
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                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG173095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
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Ratio:
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                                                                                                                                                                                                                                                     198 s 198
                                                                                                                                                                                                                                                                                           592 T 592
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus. Bukaryota; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. Barawa, T., Carninal, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Harawcto, K., Horli, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Sanai, C., Sakai, C., Sakai, C., Sakai, F., Sano, H., Sasaki, Okazaki, Y., Okido, T., Satro, R., Shinagawa, A., Takada, T., Sogabe, Y., Susuki, H., Tagani, M., Tagawa, A., Takahshi, F., Takeda, Y., Tanaka, T., Toya, T., Ritzamatsu, M. and Hayashizaki, Y. Rike Musaas Essys (Arakava, T., et al. 2001)

M. Onpublished (2001)

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Fax: 81-45-503-922
Fax: 81-45-503-922
Carninci, P., Shibata, Y., Hayatsu, M., Sugahara, Y., Shibata, K. Itoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BB653788
DEFINITION BB653788 RIKEN full-length enriched, adult male liver tumor Mus musculus CDNA clone C730026B05 5', mRNA sequence.
ACCESSION BB653788
VERSION BB653788.1 G1:16487616
                                                                                                  411 CCGCCAGCCCTGGCCCTTTTGCTACCAGATCCCCCACTTTTCATCTTTGT 460
gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT 34
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 480)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hiroacka,T., Hiroacane,T., Incoane,T., Incoane,T., Incoane,T., Incoane,T., Incoane,T., Incoane,T., Incoane,T., Incoane,T., Incoane,T., Shi Maranta,M., Nishi,K., Nomura,K., Nomno,H., Kouda,M., Matauyama,T., Satto,M., Sakai,G., Sakai,G., Sakai,T., Sakazume,M., Sasaki,D., Satto,K., Shinagawa,A., Shiraki,T., Sakazume,M., Sasaki,D., Satto,K., Shinagawa,A., Shiraki,T., Sakazume,M., Sasaki,M., Sasaki,M., Sakazume,M., Sasaki,M., Sasaki,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BBBS6627 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370035M16 5', mRNA sequence.

BBBS6627 GI:17098081
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1-7-22 Suehlro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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          265 ACAATTGCAGCCTGCTGAGAGGCCTCCCCAGCTCAGGCCTGGGGCCCCTA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGly
                                                                                                                                                                                                                                                                                                                                              67 oAlaSerProGlyProPheAlaThrArgSerProLeuPheIlePhemetA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProPr
                                                                                                                                 315 CCTCCCTACAGACAGAACCGCAA.......
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S. Grawal, T. Wake, S. Inoue, K. Togwa, Y. Tsawa, M., Ohara, E., WathNiki, M., Toneda, T., Ishikawa, T., Ozawa, K., Tanaka, T., MatSuura Hayashizaki, Y.

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                                                                                                                                                                                                                                                                                                                                                                  Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawal,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 ATGCCCAAGCAACCTTCTGATGTAGTTCTGAGTGTGACAGAAGGTGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaLysGlnProSerAspvalSerSerGluCysAspargGluGlyAr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 gGlnLeuGlnProAlaGluArgProProGlnLeuArgProGlyAlaProT 34
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Gaps: 2
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="liver tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BB653788 from: 1 to: 684
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ORIGIN
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583

EST 26-OCT-2001

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Email: genome-resigns.citken.go.jp,
UKL:http://genome.gsc.citken.go.jp/
Carninci,P., Shibata,Y., Hayatana,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Hayatana,W., Sugahara,Y., Shibata,K., Itoh
W., Konno,H., Okazaki,Y., Hurmantsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
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Wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
Shibata,K., Itoh,M., Carninci,P., Sugahara
Sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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encyclopedia: real-time sequence clustering for construction of a
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Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Squences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (Dascs 1 to 620)

8 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hirandoto,K., Horli,F., Ishili,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki,C., Sakai,C., Sakai,K., Shibata,K., Shibata,Y., Taqawa,A., Takabahi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatu,M. and Hayashizaki,Y., et al. 2001)

Inpublished (2001)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib-*RIKEN full-length enriched, 16 days neonate
              BB631162 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone Al30059E14 5', mRNA sequence.
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                                                                                                                                        BB631162.1 GI:16467982
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

'X. and Hayashizaki, Y.

'X. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) further details.
Tel: 81-45-503-9222

Exa: 81-45-503-9216

Exail: qenome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp/
Cardinci.P., Shibata.Y., Hayatsu,N., Sugahara,Y., Shibata.K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full:langth cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yonedda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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US-09-508-832-10 x BB856627
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BASE COUNT ORIGIN

FEATURES

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/tissue_tissue, libitary constructed by tiste
/tissue, libitary con
Eukaryota; Wetazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 912)

S. NIH-MCC http://mgc.nci.nlh.gov/.

NIH-MCC http://mgc.nci.nlh.gov/.

NIH-MCC http://mgc.nci.nlh.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nlh.gov

Tissue Procurement: Lofter Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1731 row: m column: 23

High quality Sequence stop: 747.
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Gaps: 4
Percent Identity: 46.626
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US-09-508-832-10 x BI555336
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LOCUS B1555336
DEFINITION 603236095F1 NIH_CGAP_Nam3 Mus musculus cDNA clone IMAGE:5289406 5',
342
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Percent Identity: 46.626
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383

63

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Homo sapiens
Eukaryota; Melazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Bummalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 64)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Nupublished (1997)

Contact: Robert Strausberg, Ph.D.
Emali. cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400F from Gibbo
High quality sequence stop: 458.

Localin/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW629314 664 bp mRNA linear EST 31-MAR. hi56e02.xl Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976314 3' similar to TR:043522 043522 BIML. [1] ;; mRNA
                                             84 rgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
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                                                                                                                                                                                                                                         34 hrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnH1sGlyGly 50
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  to reverse of: A1971169 from: 1 to: 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Progratation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 712 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:

LOCUS A1971169

DEFINITION W.24h12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2488679 3'

SIMILAR tO TR:043522 043522 BIML. [1];, MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bomo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhinl; Hominidae; Homo.

1 (bases 1 to 492)
MCI-CGAP http://www.ncbl.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Oppublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabs-refmail.nih.gov
Tissue Procurement: Mtchael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                             134 etArgGlnAlaGluProAlaAspMetArgProGluIleTrpIleAlaGln 150
                                                                                                                         481 TGGAGAATCTTAACCAA..........GTGGCACAA 506
117 oSerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerM 134
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Percent Identity: 53.435
                                                                                                                                                                                      151 GluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyr 163
                                                                                                                                                                                                                                      507 AATATCCAC .....GGTGAT ......GCCTGGTAC 530
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/clone="IMAGE:2488679"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A1971169.1 GI:5767995
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US-09-508-832-10 x AI971169/rev
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Ratio: 4.786
Percent Similarity: 53.435
                                                                                                                                                                                                                                                                                      seq_name: gb_est1:A1971169
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BASE COUNT ORIGIN

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

FEATURES

EST 31-MAR-2000

8

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tracer in a subtractive hybridization reaction. The driver was PCF amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 72996-731399. Subtraction by Bento Sources and M. Fetime Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 ACANGAGGCACAA......548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 ...... 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 erSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAspThrAsp 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 .. AlaSerMetArgGlnAlaGluProAlaAspMetArg... ProGluIle 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   548 ..... 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 euGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGlyGluGly 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 rProGlyProPheAlaThrArgSerProLeuPheIlePheMetArgArgS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AspSerCysProHisGlySerProGlnGlyProLeuAlaProProAlaSe 69
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ORIGIN
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147 TrpileAlaCln 150 |||:::|||::: 394 TGGTTAGCAAA 383